

FIGURE 1

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCTCAGGAGGTGCCTCCAGGCGGCAGTGGGCTGAGGCCCCAGC
AAGGGCTAGGGTTCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCTGGGC
TCAGCAGCATCAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCACCAACCCGGAGG
AGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCGCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGTGTGATGTGGCT
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCGCTACCGGCCCGGCCGTTAGGGTGTGTGCT
GTCCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTTCGTGCACGCTGTGTACAGCCCTTC
TCACCACCTGCGACGGGCACCGGCCCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC
CGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGTGTCGCCCGGCTGGAAGAG
GACCACGGGCTTCCTGGGGCTGTGGAGCAGCAATATGCCAGCCGATGCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCAGTGTAGGAGGGCGGCTGTCCCAGCGCTGCATCAACACCGC
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCAAGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGACAGTGAATGAAG
GAAGAAGTGACAGAGGCTGCAGTCCAGGGTGGACCTGTGAGGAGGAAGCTGCAGCTGTGTCT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGACCCCGGAGCC
TCCTGGTGCACCTCCTTCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTCTC
CTGGAGGAGCAGCTGGGGTCTCTCTCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGG
CTGGACTGAGCCCTCAGCCCGCTGCAGCCCCCATGCCCTGCCAACATGTGGGGGTCTC
CAGAAGCCACCTCGGGGTGACTGAGCGAAGGCCAGGCAGGGCTTCCTCCTTTCTCTCTC
CCCTTCCTCGGGAGGGTCCCCAGACCTGGCATGGGATGGGCTGGGATTTTTTTGTGAAT
CCACCCCTGGCTACCCCCACCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA
GCTGAGGGAAGGTACGAGTTCCCTGTCTGGAGCCTGGGACCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCTCAGTGGGGCTGTGCTGCTGACCCCCAGCACAAATAAAATGAAA
CGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCGCGACTCT
AGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTGTATTATGCAGCTTATAATGGT
TACAAAT

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FIGURE 2

MTDSPPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV
SESEFVQRVYQPFLLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLEGAC
GAAICQPPPCRNGGSCVQPGRCRCPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSADGTLCPVKGPPRVAAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAFLHSLAS
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

10976373-109801

FIGURE 3

CGCTCGCCCCGTCGCCCCCTCGCCTCCCCGCAGAGTCCCCCTCGCGGCAGCAGATGTGTGTGGG
GTCAGCCCCACGGCGGGGACTATGGTGAAATTCCTGGCGCTCAGCAGCTACTGGCCCCCTGATC
CGGTTCTTTGGTGCCCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCCTTGAA
CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTGCAGATGCTGGGCCAGCTACGGGCTGGCGT
ACTCCCTCATGAAGTCTTTCACGGGTCCCATGAGTGACTTCAAAAATGTGGGCTGGTGT
GTGAACAGCAAGAGAGACAGGACCAAAGCCGCTGCTGTGTATGGTGGTGGCAGGGCCATCGC
TGCCGTCTTTACACACTGATAGCTTATAGTGATTAGGATACATATTCAATAAACTGC
ACCATGTGGACGAGTCCGTGGGGAGCAAGACGAGAAGGGCCCTTCTGTACTCTCGGCCCTTT
CCTTTCATGGACGCAATGGCATGGACCCCATGCTGGCATTCTCTTAAAAACACAATACAGTTT
CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTTGTAGCCATTTTGC
TTCACAGTCACCTGGAATGCCGGGAGCCCTGCTCATCCGATCCTCTCCTGTACATGGG
GCATTGTGCGCTGCACCAACCTGTGCTGGGCTACTACAAGAACATTCACGACATCATCCC
TGACAGAAGTGGCCCCGGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT
GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCGGGACCTTGGTGGCATTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGATCCTGCTTCG
ACAAGAATAAACCCAGCAACAAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCACATC
AAGAAGTTCACTTTCGTCTGCATGGCTCTGTCACTCAGCTCTGTTTTCGTGATGTTTGGAC
ACCAACGTTCTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCCTTTGCAGAAC
TCTGTGTTGTTCTTTTGGGATCTTCTCCTTCTTCCAGTTCAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGCTCTTGCCTCCAGCTCTGTGTCGG
GATCATCGTCTCATCGCCAGCTCGTGGTCTACCTACCTGGGGGTGACGGTGCAGCCC
TGGCGTGGGCTCCCTCCTGGCGGGCTTGTGGGAGAATCCACCATGGTCCGCATCGCTGCG
TGCTATGTTACCGGAAGCAGAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGAAGA
CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAGG
AGAATGAATAAGGCACGGGAGCCATGGGCACTGAGGGACGGTCAGTCAGGATGACACTTC
GGCATCATCTTCCCTCTCCCATCGTATTTTGTTCCCTTTTTTTTGTGTTTGGTAAAT
GAAAGAGGCCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACAT
GACGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTA AAAACAAACGAAACAACTGAC
TTCATAACCCCTGCCTCAGCAAAACCCAAAAGACACAGTCGCCCTCACGGTTGACGTTGTGTC
TCCCTCCCCTGGACAACTCCTCTTGGAACCAAAGGACCTGAGCTGTGCCATCGCGCTCCGT
CACCTGCAACGAGGCCACGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAAATCAACAGG
TTAAAACTCGGCTTCTTTGATTTGCTTCCAGTCACATGGCCGTACAAAGAGATGGAGCCC
CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACATGACG
GAGGCGGGTGGCACGCTGCAGCCCGAGTCCCGGTCACACTGAGGAACGGAGACCTGTGAC
CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAATGCCCGGG
GGCAGCAAACTGCATGGTTGAATGATAGCATTTCCTCTGCGTTCTCCTGATCTGAGCAA
GCTGTGAGTTCTCACCCCCAGCTGTATATACATGAGCTAACTTTTTTAAATTTGTCAAAA
GCGCATCTCCAGATTCCAGACCTGCCGATGACTTTTCTGAAGGCTTGCTTTTCCCTGCG
CTTTCTGAAGTTGCGATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCAATTTGTGACT
TACAGTGAAGTGAAGCTTTAAGTCTCATCCAGCATCTAATGCCAGGTTGCTGTAGGGTAAC
TTTTGAAGTAGATATATTACTGGTTCTGTATCTTTAGTCATAACTCTGCGGTACAGGTAA
TTGAGATGTACTACCGTACTTCCCTCCCAACACCATACGATAAAGCAAGACATTTTATAAGC
ATACCAGAGTCATATGTGGTCTCCTCGTAAATAACGCATTCGAATCCATGCAAGTCAGTA
TATTTTTCTAAGTTTGGAAAGCAGGTTTTTCTTTAAAAAATATATAGCAACGGTTCACT
AAATGAGTTTGTGAGAAATCCTAGACTGAAAGAACCTAAACAAAAAATATTTAAAGATA
TAAATATATGCTGTATATGTTATGTAATTTATTTAGGCTATAATACATTTCTATTTTCG
ATTTTCAATAAAATGTCTCTAATACAAAAA

FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSDFKNVGLVVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSIDLGYIINKLHHVDES
GSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFAILLHSHLEC
REPLILPILSLYMGALVRCTTLC LGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQRISRPIVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNPNPSN
KLVSTSNVTAAHIKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFELCVVPLR
IFSFFPVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVLPYLVGHGATLVGGSLL
AGFVGESTMVAIAACYVVRKQKKKMENESATEGEDSAMTDMPTTEEVTDIVEMREENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,
408-423, 431-445

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FIGURE 5

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAATCCGTGCTGTGTATCCTGCTTTCG
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCCAGGCGGCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGNAAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGAGAAC
TCTGTGTGTTCTTTGCGGATCTTCTCCTTCTTCCAGTTCAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

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FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG
GAGCAGGGCAAAACAGTNACGGGCAGCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCTTTGCGGATTTTCT
CCTTTTTCCCAGTTCAGTCACAGNGAGGGCGCATCTCACCGGNGGNTGATGACANTGAAG
AAAACCTTTGTCTTGCCCCAGCTNTTTGGTGCGGATCATTGTCTNATNGCCAGCCTTGT
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

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FIGURE 7

TATTCCAGTTCGGTCA CGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA
ACCTTNGTCCTTGCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATGCCAGCCTNGTGGT
CCTACCCTACCTGGGGGTGCACGGTGAGAC

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FIGURE 8

GCCCCGCGCCCGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA
GCCTGCTCCCTGCTCAGCTGCGGCTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG
CTGTGCCCCCGCAGCCGCAACTCCACCGTGAGCGGCCTCATCTTCACGTTCTTCTCTCTCC
TGGGGGTGCTGTTGTCCATCATTATGCTGAGCCCGGGCTGGAGAGTCAGCTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCTTGACGGGCCATCGACTGTGG
CTCCCTGCTTGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTCTCT
TCTTTTTACCCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCGGGCTGCCATCCAG
AATGGGTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCTCTTCA
TCCTCATCCAGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC
AAGGCCGAGGAGTGCATATCCCGTGCCCTGGTACGCAGGCCTCTTCTTCTTCACTCTCTCTT
CTACTTGCTGTGCATCGCGGCCGTGGCGCTGATGTTCTACTACACTGAGCCCGAGCGGT
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT
GCTGTCTGCCCCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGTCTGAGGCTCGGTCTCAT
CACCTCTACACCATGTTTGTCACTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCATTTGCCAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCCGAGCATTGTGGGCCTCATCATCTTCTCTCTGTGCACCTCTT
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC
TTTGACAACGAGCAGGACGGCGTCACTACAGCTACTCCTTCTTCCACTTCTGCTGGTGCT
GGCCTCACTGCACGTATGATGACGCTCACCACTGGTACAAGCCCGGTGAGACCCGGAAGA
TGATCAGCACGTGGACCGCGGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCTCTC
TACCTGTGGACCTGGTAGCCCCACTCCTCTGCGCAACCGCACTTCAGCTGAGGCAGCCT
CACAGCCTGCCATCTGGTGCTCTCTGCCACCTGGTGCTCTCGGCTCGGTGACAGCCAACCT
GCCCCCTCCCCACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCGACTCCAGGACCTG
CCCCCTGAGCCGGGCCTTCTAGTCGTAGTGCCCTTCAGGTCGAGGAGCATCAGGCTCTGCA
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCTCCCTCTCTCTCTGT
TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGG
CTGTGAGAGAGCGGGGAACCTCCACCAAGTGGGGCATCCGGCACTGAAGCCCTGGTGTT
CCTGGTCACGTCCCCAGGGGACCTGCCCCCTTCTGGACTTCGTGCTTACTGAGTCTCT
AAGACTTTTTCTAATAAACAAGCCAGTGCCTGTAAAAA

0978375-101601

FIGURE 9

MGACLGACSLSCASCILCSGPCASRNSTVSRLLFTFFLFLGVLVSIIMLSPGVE
SQLYKLPWVCEBEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFTLLMLCVSSRD
PRAAIQNGFWFFKFLILVGLTVGAIFYIPDGSFTNIWFYFGVVGSLFILIQLVLLIDFAHSW
NQRWLGAEECDRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHGKVFISLNLTFC
VCVSIAAVLPKVQDAQPNISGLLQASVITLYTMFVTWSALSSIEQKCNPHLPTQLGNETVVA
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA
ACEGRAFDNEQDGVITYSYFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVWKICAS
WAGLLLYLWTLVAPLLLRNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

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FIGURE 10

GAGCGAGGCCGGGACTGAAGGTGTGGGTGTGAGCCCTCTGGCAGAGGGTTAACCTGGGTC
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCGCGAGGACTTGA
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAGAAGGCCATGGAGGTGCCGCCACCGGC
ACCGCGGAGCTTTCTCTGTAGAGCATTTGTGCCTATTTCCCGAGTCTTTGCTGCCGAAGCTG
TGA CTGCCGATTTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCAGAGCCC
TATTACCCGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG
TGTATGGGGGAATACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT
CATTTCGTTATGGCTGGCGCTGGGGTTGGAGAAGTGCAGTGTTTGTGACTATATTCAACACAG
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAATTGCAGGA
GCTGTACCGGAAGTCTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCTGCTGATGGCATTTCAGAAGTACGCTG
GTGAGACTGTTTCAGGAAAGAAAACAGAAGGATCGAAAGGCACCTCCATGAGCTAAAACTGGAA
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCTAGAAACC
CTTCAGTAATAGATAAAACAAGACAAGGACTTGAAAGTGCTCTGAACCTTGAAACTCACTGGAGA
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGCTCTTTTCTTTTCTT
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA
GCAGTAAATAAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

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FIGURE 11

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQVIEQSQAEIYHNRFDVQSAH
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSFLFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPNPSVIDKQDKD

Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

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FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGTTTCATG
GCTGGCGCCGAACC

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FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCCTATTTCCCGAGTTTTTGTGCGCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

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FIGURE 14

GAGCCGCCGCCGCGCGCGCCGCGCACTGCAGCCCCAGGCCCGGCCCCACCCACGTCT
GCGTTGCTGCCCGCCTGGGCCAGGCCCCAAAGGCAAGGACAAAGCAGCTGTCTCAGGGAACTT
CCGCCGGAGTCGAAATTACGTGCAGCTGCCGGCAACCACAGGTTCCAGAGATGGTTTGC GG
GCTTCGCGTGTTCGAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTG
CTGCTAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT
CGGCGTGGTCATTGCAGTGGGCATCTCTTGTTCCTGATTGCTTTAGTGGGTCTGATTGGAG
CTGTAAACATCATCAGGTGTTGCTATTTTTTATATGATTATCTGTTACTTGTATTTATT
GTTCACTTTTCTGTATCTTTCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT
GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT
GTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCAC
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTGGAGATTGTTGG
TGGCATTGGCCTGTTCTTCAGTTTACAGAGATCCCTGGGTGTTTGGCTGACCTACAGATACA
GGAACCGAAAGACCCCCGCGCAATCCTAGTGCAATCTCTTTGATGAGAAAAACAAGGAAGAT
TTCCTTTCGTATTATGATCTTGTTCACCTTCTGTAATTTCTGTAAAGCTCCATTGCGCAGT
TTAAGGAAGGAAACACTATCTGGAAGTACCTTATTGATAGTGAATTATATATTTTTACT
CTATGTTTCTCTACATGTTTTTTTTCTTTCCGTTGCTGAAAAATATTTGAACTTGTGGTCTC
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTATTGTCGGGCACTGTCCACTGTGGCCTT
TCTTAGCATTTTACCTGCAGAAAACTTTGTATGGTACCAGTGTGTTGGTTATATGGTGAA
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTCTCTAC
TGGAAAAAGAGTGGAAATTTATTAAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA
TCCAAATCCCAATTTTTTTTGGTCTTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTAGTA
TAAAAATGATAATTTACTTGTAGTCTTTATGATTACCAATGTATTCTAGAAATAGTTAT
GTCTTAGGAAATTTGGTTTTAATTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGGTTT
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCTCCATCAGAATGGAACGAGTTT
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTATAATAAATTTGAAGCTAA
AAGACTGCATTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGATATTG
ATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTT
GTCAAACCTAAGCATATTTGAATATGATCTCCCATAAATTTGAAATTGAAATCGTATTGTGTG
GCTCTGTATATTCTGTTAAAAAATTAAAGGACAGAAACCTTTCTTTGTGTATGCATGTTTGA
ATTAAGGAAGTAATGGAAG

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FIGURE 15

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIavgIFLFLIALV
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQGQLLEVGNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRfVGGIGLFFSFTEILGVWL
TYRYRNQKDPANPSAFL

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

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FIGURE 16

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTATATGATTATTCTGTAANT
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCTAATGACACCTGTNTGGCTAGCTGTGTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTGA
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCAG

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FIGURE 17

AATCCCAAATCCCCAATTTTTTTGGNCTTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT
TAGTATAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG
TTATGTCCTTAGGAAATTGTGGTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG
TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
CCACTTGC

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FIGURE 18

ATGATTATTCTGTTACTTGTATTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCGGAAGTGTTAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA
TCATAGGAGAATATGC

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FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTGTAGACGCTGCAGTGTGAGGGACCTGT
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCCCTACACTTTTTCAGTGAACCTTCCACCTGATTGTGTCTATGACTGGCTG
ATCCTCCAAGGTCAGCCCAAGCCAGTTTGTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC
CCGGGCCCTAACAGGGAATTTCCATCACCGTGGTACAAAGGCAGACAGCGGGCACTACCAC
TGCACTGGCATCTTCCAGAGCCCTGGTCTCGGGATCCAGAAACAGCATCTGTTGTGGCTAT
CACAGTCCAAGAACTGTTTCCAGCGCCAATTTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCCTGAGTTGTGAGACAAAGTTGCCCCCTGCAGAGGTCAGCTGCCCGC
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCACTAGTGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTTGGAAACAGAGCCCCAGCTAGAGATCAGAGTGCAGGCTGCTTCCAGTCT
GCTGCACCTCCACATTGAATCCAGCTCCTCAGAAATCAGTCTCCAGGAACCTGCTCCTGA
GGAGGCCCTGGGCCCTCTGCCTCCGCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG
CAGGATGTGAGAGTCTCTCTCGTCACTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAAGTAAACAGTTTCATCCATGATCTCACT
TAACCACCCCAATAAAATCTGATTCTTTATTTTCTCTCTCTCTGCTGCACATATGCATAAGTA
CTTTTACAAGTTGTCCAGTGTGTTGTGTAGAAATAGTAGTTAGGTGAGTGTAAATAAATTT
ATATAAAGTGAGAAATAGAGTTTAGCTATAATTGTGTATTCTCTCTTAAACACACAGAAATTC
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAAATGTTGTGATTTAAAGAGAA
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGTTGGGGGATGGTGGGATGT
GTGTCCTAGTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG
GGCAGTACCCCAACGAAATAATCTGGCCCAAATGTCAAGTTGTACTGAGTTTGAGAAA
CCCCAGCCTAATGAACCCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT
TATCTCTTTCCAGCCTCATTGAGCTATTCTTACTGACATACCACTCTTTAGCTGGTGGCTATG
GTCTGTTCTTTAGTTCTAGTTTGTATCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC
AAGGTGATGGCATTAGAAGTGGGCCCTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTACCCCTTCCACCAT
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAACAGCTGTGCGCAAAACCCG
ACTCTGTGTTGCCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATTTCTGG
TTGTTTGTAGCCTAA

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FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGVLVWAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAPKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSAAPTTLNPAPQKSAAPGTAPEEAPGPLPPPTPSSSEDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

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FIGURE 21

CCCACGCGTCCGCCACGCGTCCGCCACGGGTCCGCCACGCGTCCGGGCCACCAGAAGTT
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG
ATCTTACTGGGCCTGCTACTCTCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT
GGAAGTGCCAGAGAGTGTAAACAGGACCTTGGAAAGGGGATGTGAATCTTCCCTGCACCTATG
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAAACGTGGCTCAGACCCCT
GTACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAAGTACCAGGGCCG
CTGTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCCTGGAGATGG
ATGACCGGAGCCATACAGCTGTGAAGTCACCTGGCAGACTCTGTATGGCAACCAAGTCGTG
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC
TGGCAGCGGTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC
GGGGTTCTCCTCCCATCAGTTATATTGGTATAAGCAACAGACTAATAACAGGAACCCATC
AAAGTAGCAACCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTTA
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC
TTGAAAGCAACATCTACAGTGAAGCAGTCTCTGGGACTGGACCATGACATGGATGGCTACCT
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGAAGACATCCCCA
CAAGAGCATGTCTACGAAGCAGCCAGGTAAGAAAGTCTCTCCTCTTCCATTTTTTGACCCCGT
CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC
AATCCTAAGGCCGGAGGCCCTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC
AGAATCCTGGGTGGTAGGATCCTGATAAATTAATTGGCAAGAAATTGAGGCAGAAGGGTGGGA
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT
CCAGTGATGAGCCAACTTCCAGAATCTGGGCAACAACTACTCTGATGAGCCCTGCATAGGA
CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCGCTGTCTGGACACAGTTCC
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTAAAAATGCCCATTAGGC
CAGGATCTGTGACATAATTGCCTAGTCAGTCTTTCGCTTCTGACATGGCCTTCTTCCCTGCT
ACCTCTCTTCTGGATAGCCCAAAGTGTCCGCCTACCAACACTGGAGCCGTGGGATGCATCT
GGCTTTGGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACAGAGGGGAAGATG
CCCATAGCACTAGGACTTGGTCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA
CCAGAAGACCCGAGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT
TTCTCTTTCTCAGGGCCAGACAGCTTTAATTGAAATTGTTATTTACAGGCCAGGGTTCA
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA
ATCATAACAGC

09976375.101601

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLGHILTVDITYGRPILEVPESVTGPGWKGDVNLPCYDPLQGYTQVLVKWLVQRGS
DPVTIFLRDSSGDHIQQAKYQGRLVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRIQLCCQARGSPPISYIWYKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKVVKDSSKLLKTKTEAPTMT
YPLKATSTVKQSWDWTDTMDGYLGETSAGPGKSLPVFAILLIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAAR

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

FIGURE 23

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCTCCCGCCCGGCACAT
GGCTGCAGCCACCTCGCGCGCACCCGAGGCGCGCGCCAGCTCGCCGAGGTCGCTCGGA
GGCGCCCGGCGCGCCCGGAGCCAAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
GGGAATGTCCTCTCTCTCTCTCTCTGCTAGTTTCTTACTATGTTGGAACTTGGGGACTCA
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTTGCCACCACTCAACTGGGGC
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCATAATGAAGGGAACCAAAAA
GTGGTGATCACTTACTCCAGTCGTCTATGCTACAATAACTTGACTGAGGAACAGAAAGGGCCG
AGTGCCCTTTGCTTCCAATTTCTTGGCAGGAGATGCTCCTTGAGATTGAACCTCTGAAGC
CCAGTGATGAGGGCCGCTACACCTGTAAGGTTAAGAATTGAGGGCGCTACGTGTGGAGCCAT
GTACTCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCTCTGGCACAGAGCCCAATTGTGTATT
ACTGCGCAGCAATCCGAGAGAAAAGGGAGAGGATGAACGTCTGCCCTCCCAATCTAGGATT
GACTACAACCACTGGACGAGTTCTGCTGCAGAACTTACCATTGCTTACTCTGGACTGTA
CCAGTGACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACCTGTACAGT
ATGTAACAAGCATCGGCATGTTTGCAGGAGCAGTGACAGGCATAGTGCTGGAGCCCTGCTG
ATTTTCTCTTGGTGGGCTGCTAATCCGAAGGAAAAGCAAGAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAGCCCGCTCTGTGAAACCCAGCT
CCTCTTCTCAGGCTCTCGGAGCTCAGCTCTGTTTCTTCTCCACTCGCTCCACAGCAAT
AGTGCTCAGCGAGCCAGCGGACACTGTCAACTGACGCGAGCACCCAGCCAGGGCTGGCCAC
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
CTAATCTGACCAAGCAGAAACCAACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA
ACGGTCTGAATTACAATGGACTTGACTCCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTC
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCCAGATGAGAGGTCTCTAAGTAGCA
GTGAGCATTGCACGGAACAGATTGAGATGAGCATTTTCTTATAACAATCCAAACCAAGCAAA
AGGATGTAAGCTGATTCTCTGTAAGAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTGTATCAGTGCTTTGATTCACAAT
TTCAAGAGGAAATGGGATGCTGTTGTAAATTTCTATGCAATTTCTGCAAACTTATTGGATT
ATTAGTTATTGAGACAGTCAAGCAGAAACCCAGCCTTATTACACTGTCTACACCATGTAC
TGAGCTAACCACTTCTAAGAAACTCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TTCATTTGTATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC
TATGAAAGGAGACAAAATTTGTGACAAAGGATTTGGAAGAGCTTTCCATCTTCTATGATT
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTCAAT
CAGATGCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAATAACAACATGTCATT
TATCAACGTCTTAGAAAGAAATTTCTTAGAGAAAAGGGATCTAGGAATGCTGAAAGATTA
CCCAACCACTTATAGTCTCTTCTTCTGAGAAAATGTGAACACAGAATTGCAAGACTGG
GTGGACTAGAAAGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
ATTGCACTCCAGCTGGGTGACAGAGCGGGACTCCGTCTC

0978375 101601

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELETEGSDLTLCESSSSGTEPIVYVWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPVVRGSEPKKVHHANLTKAETTPSMIPSQSRAFAQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

09/03/95 10:50:14

FIGURE 25

GTGGTTCCTTTGGCTCTCTCGCGCCCACTCCTCCTCGGTTCTCTCAGCCGCTGTGCGGAGGAGACACCCGGA
 GACGCGGCTGCACTGCGCGGCTCTCTCCCGCTCGGCGGCTCGCGCTGGGCAAGTGTGAGCGCCCTAG
 AGCCCTCTCTCGCGCTCCTCTCTCTCGCGGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG
 CCGCGGAGCGCGCGGTGGATGCGGGCTGGGCGAGAAGCAGCCGCGATTCCAGCTCCCGCGCGCCCGCGGCG
 CCCCCTGGAGTCCCGGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCTCCTCGAGCGCATC
 GCCCGCGAGCCACAGCCAGATGATCGCGGCTCCTCTCTCTGTTGGATTCTTAGCACCACAGCTCAG
 CCAGAACAGAAAGCCCTCGAATCTCATTTGGCACATACCGCCATGTGACCGTCCACCGCCGACAGCTGCTAACCTGT
 GACAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCTCTGCGGCTCGCAGAGTGTGCCCT
 GTGGGGAACCTTTACAGGACATAGAAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGGCAATG
 ATTGAGAAATTAACCTTTGTGCTGCTTGTACTGACCGAGAAATGCATCTGCCACCTGGCATGTTCAGTCTAACGCT
 ACCTGTGCCCCCATACGGTGTGTCTCTGTGGTTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG
 TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTCTAGTGTGATGAAATGCAAGCATACACAGACTGT
 CTGAGTCAGAACCTGGTGGTGATCAAGCCGGGACCAAGGAGACAGACAACGCTCTGTGGCACACTCCCGCTCTC
 TCCAGCTCCACCTCACCTTCCCTTGGCACAGCATCTTTCCACGCTCTGAGCACATGGAAACCCATGAAGTCCT
 TCCTCCACTTATGTTCCCAAGGCATGAACTCAACAGAAATCCAACTCTTCTGCTCTGTTAGACCAAGGTAAGT
 AGTAGTCTCCAGGAGGGAAGTCCCTGACAAACAAGCTCAGCAAGGGGGGAAGGAAGAGCTGAAACAAGCCCTC
 CCAAACTCTCAGGATGTCAACACACAGCAAGGCCCCACACAGACATCTGAACTGTCTGCGCTCCATGGAG
 GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGGCCCAAGAGGGGACATCTAGACAGAACCTACACAAG
 CATTTTGACATCAATGAGCATTTGCCCTGGATGATTGTGCTTTTCTGCTGCTGGTGCTTTGTGGTGATTGTGGT
 TGCAGTATCCGAAAAGCTCGAGGACTCTGAAAAAGGGGCCCGCGCAGGATCCAGTGCCATTGTGAAAAGGCA
 GGGCTGGAAGAAATCATGACTCCAAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
 ATCCTGAGCTGTAGCAGCCCAAGTGGGAAGCGAGTGGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG
 AGGGAGGTTGCTGCTTTCTCCAATAACTTACAGCCGACCCAGAGCGGGCTACGCGAGCTCTGCAAGCATGGAAC
 ATCCGGGGGCGCGAGGCGCTCGCCAGCTTAATTAGCGCCCTGCGCCAGCACCGGAGAACGATGTTGTGGAG
 AAGATTCTGGGCTGATGGAAGACACCAACCCAGCTGGAACCTGACAACTAGCTCTCCGAGTGAGCCCCAGCGCG
 CTATAGCCGAGGCCCATCCCGACGCCCAACGCGAACTTGAGAAATCCGCTCTCTGACCGTGGAGCCTCCCCA
 CAGGACAAGAACAGGGCTCTCTCGGTGATGAGTCGGAGCCCTTCTCGCTGCTGCTGCTACTACTACTAGCCGCTCC
 TCCGCGCTGAGCAGGAACGGTCTCTTTATTACCAAGAAAGAGACGACAGTGTTCGCGAGGTATCGCTCGGAGC
 CCCTGTGACTGTCAGCTACTCTTTGATGACATGCTCCACTTTCTAAATCTGAGGAGCTCGGGTGTATGAGAG
 ATTCCAGGCTGAGGACAACTAGACCGGCTATTGCAAAATATTGGAGTCAAGAGCCAGGAAGCACGACAGACC
 CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGATAGTGCATTCTGAAATTAATCA
 ATTTAGTGGCAGGCTGGTTTTTAATTTTCTCTGTTTCTGATTGTTGTTGGGGTGTGTGTGTGTTGTTGTTG
 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTTAAACAGAGAATATGGCAGTGCTTGAATCTTTCTCTCTCTC
 TCTCTCTTTTCTTTTAAATAACTCTTCTGGGAAGTTGGTTTTATAAGCCCTTTGCCAGGCTGAACTTTGTGAA
 ATACCACCACTAAAGTTTTTAAGTTCATATTTCTCCATTTTGCCCTTCTATGTATTTTCAAGATTATTCTG
 TGCACCTTTAAATTTACTTTAACCATAAATGCAGTGTGACTTTCCACACACTGGATTGTGGGCTCTTAAC
 TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTATGTCTCTTAAACATTACACCTACTTTTT
 AAAAAAATAATATTACTATTTTATTATTGTTTGTCTTTATAAATTTCTTAAAGATTAGAAAAATTTAAGA
 CCCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTAAATATGTCTTGTATAGTTATATATCATGG
 CTGAAACTGACCAACATATTGCTGATTGTATGGTTTTCACTGGACACCGTGTAGAATGCTTGAATTTACTGTAC
 TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCTCAAGCCATCAGGATTGCTATTTAAGTGGCTT
 GACAACTGGGCGCCCAAGAACTTGAACCTTCACTTTTAGGATTTGAGCTGTGTTCTGGAACACATTGCTGCACTTT
 GGAAAGTCAAATCAAGTGGCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTTG
 TTTTATATACACATAATCAATAGGTCCAATCTGCTCTCAAGGCTCTGGCTGGTGGGATCTCTTCAACAAAT
 ACTTTAAATTAAGTGGCTGCACTGTAAGAACCCCTGTCTGATATATTGCAACTATGCTCCATTTTAAAGAT
 TACCTTTTAATGCTCAGTTTGGCGGTTCCAATGCAAGAGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTGTGG
 GTAGTGGTGAAGGACGATATCAGAAAAATGCCTTCAAGTGACTAATTTATTAATAAACATTAGGTGTGTGTTA
 AAAAAAAA

00978375.101601

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594
><subunit 1 of 1, 655 aa, 1 stop
><MW: 71845, pI: 8.22, NX(S/T): 8
MGTSPSSSTALASCRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATG
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCA
ALTDRECTCPPGMFQSNATCAPHTVCPVGVGVRKKGTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKKHFDINEHLPWMIVLFLLLVLVIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMPTPTQNRKWIYYCNGHGIDILKLVAQVGSQWKDIY
QFLCNASEREVAAFSNGYTADHERAYAALQHWITIRGPEASLAQLISALRQHRRNDVVEKIRG
LMEDTTQLETDKLALPMSPLSPSPSPNAKLENSALLTVEPSQDKNKGFFVDESEPLL
RCDSTSSGSSALSRRNGSFITKEKDDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDRLFEIIGVKSQEASQTLLDSVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

0978375-101501

FIGURE 27

ATGGAAGCCAGTAACACTGTGGCCTACTATCTCTCCGTGGTGCCATCTACATTTTTGGGA
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTGAGAGGTCTCGAAATAGTCAC
CATGGGGGAAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTGGCC
TTGATGATTTGAAAAAAGTCCGTGTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG
TCACTGCTGCCATTGAAGTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCCGTCACTCCT
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC
GAGTACCGCTGTGTCCGGGTGGGTGCTCAGAATGCCGTGCTCCAGGTGTTCCACAGCTGCTTC
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCTCTGTCCTAAC
TGGGTTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCGAGTTC
CGGGAGGAGTGTGTGTCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCAAGTGGTTACCTTGCAGTGCACAGCCT
GTGGTCTAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAACATGTCCTTGCTCTCGCAG
TGGCCCTGGCAGGCCAGCCTTCAGTTCCAGGGTACCACTGTGCGGGGGCTCTGTGCATCAC
GCCCTCTGGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA
CCATCCAGGTGGGTCTAGTTTTCCCTGTTGGACAATCCAGCCCCATCCCACTGGTGGAGAAG
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCTGCCCACTCTGAAGAGA
ACTTCCCCGATGGAAAAAGTGTGCTGGACGTCAAGGATGGGGGGCCACAGAGGATGGAGGTGAC
GCCTCCCTGTCTGAAACACGCGGCCGTCCCTTTGATTTCACAAGATCTGCAACACAG
GGACGTGTACGTTGGCATCATCTCCCTCCATGCTCTGCGCGGGCTACCTGCACGGGTGGCG
TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG
TTAGTGGGAGCGACAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGGTGTACAC
CCGTGTCACTCCTTCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA
GAGGAAGGGGACAAGTAGCCACCTGAGTTCTGAGGTGATGAAGACAGCCCGATCCTCCCT
GGACTCCCGTGTAGGAACCTGACACAGCAGACACCCCTTGGAGCTCTGAGTTCGGGCACCA
GTAGCAGGCCCCGAAAAGAGGCACCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTTT
GTTTTTTGTTTTTTGAGGTGGAGTCTCGCTCTGTTGCCCGAGGTGGAGTGCAGTGGCGAAA
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTGCTCAGCTTCCCCA
GTAGCTGGGACCACAGGTGCCCCGCCACCAACCCAACTAATTTTTGTTATTTTTAGTAGAGAC
AGGGTTTACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT
CAGCCTCCACAGTGTCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCAGCTCCTTTC
TGATCTTCACTAAGAACAAGAAAGCAGCAACTTGAAGGGCGGCCCTTCCCACTGGTCCAT
CTGGTTTTCTCTCAGGGTCTTGCAAAATCTCTGACGAGATAAGCAGTTATGTGACCTCAGC
TGCAAAAGCCACCAACAGCCACTCAGAAAAGACGCACGCCAGAAAGTGCAAACTGCACTC
ACTGCACGTTTTTCATCTCTAGGGACAGAAACCAACCCACCTTTCTACTTCCAAGACTTAT
TTTCAATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAAGCCCTATTTTCATCTATTTCTT
TGTAGCATTTGGTGTCTGACGTATTATTGTCTTTGATTGCAAAATAATATGTTTCTTCCCT
CATGTCTGGCGTGTCTGCTGGACTGGTGAAGTGAATCAAATCATCCACTGAAA

097875.101601

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAAS
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKVLTALHH
SVYVREGCASGHVVTILQCTACGHRRGYSSRIVGNGMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIITAAHCYVDLYLPKSWTIQVGLVSLDNPAPSHLVEKIVYHSHKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHR
DVYGGIISPSMLCAGYLTGGVDSCQGDSSGGLVQCERRLWKLVGATSFSGIGCAEVNKPVGYYT
RVTSFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

09978375.101601

FIGURE 29

CCCACGCGTCCGTCTAGTCCCGGGGCCAACTCGGACAGTTTGCTCATTTATTGCAACGGTCAAGGCTGGCTGT
 GCCAGAACCGCGCGCGCGCGCACGACGACACACACGCGGGGAAACTTTTTAAAAATGAAAGGCTAGAGA
 GCTCAGCGCGCGCGCGGGCGCTCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCCGCA
 GCGCCGCGCCCCGGCTCGCGCGCCGCGTGGATGGTGACGCGCTCGCCCGCGGCCGAGAGCTGCTGCATGAAG
 GCGCGGCACAGTatgCGAGCGCGCGCGCTGCCGTGTCCCCGCCCGCGCCCTCTGTCTCGCCCTGCGCGGCTCTCT
 GCTCGCGCCCTGCGAGGCGCGAGGGGTGAGCTTATGGAAACCAAGGAAGAGCTGATGAAGTTGTCAGTGCCTCTGT
 TCGGAGTGGGGACCTCTGGATCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGTGAATATTCGACT
 ACAACGGGAAGACAAAGAACTGATCATAAATCTGGAAAGAAATGAAGGTTCTATCTGCGACAGCTTCCAGGAAC
 CCACTATCTCGAAGACGGTACTGATGTCTCCCTCGCTCGAAATTAACAGGGTCACTGTTACTACCATGGACATGT
 ACGGGGATATTCTGATTTCAGCAGTCACTCTCAGCAGGTGTTCTGGTCTCAGGGGACTTATGTGTGTTGAAATGA
 AAGCTATGTCTTAGAACCAATGAAAGTGCAACCAACAGATACAACTCTTCCAGCGAAGAGCTGAAAGCGT
 CCGGGGATCATGTGGATCATCATCAACACACCAAACTCTGCTCGAAAGAATGTGTTCCACCACTCTCAGAC
 ATGGGCAAGAAAGGCATAAAAGAGAGACCTCAAGGCCAACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAACCG
 AGAGTTTCAGAGGCAAGGAAAGATCTGGAAAAAGTTAAGCAGCGATTAATGAGATGTCTAATCAGCTTGACAA
 GTTTTACAGACCACTGAACATTCGGATCGTGTGGTAGGCGTGGAACTGTGGAATGACATGGACAATGCTCTGT
 AAGTCAGAGCCCTTACACAGCTCATGAATTTCTGAGTGGAGGAAGATGAAGCTTCTACCTCGCAATCCCA
 TGACAATTCGCGAGTTGTCACTGGGGTTTATTTCCAAAGGACCACTCATCGGATGGCCCCAATCATGAGCATGTG
 CACGCGCAAGCAGCTGTGGGGGAATTTGTCATGGACCACTCAGACAAATCCCTTGGTGCAGCCGTGACCTGGGCACA
 TGAGCTGGGCCAAATTTCCGGATGAATCATGACACATGGACAGGGGCTGTAGCTGTCAATGGCGGTGAGAA
 AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCATGGTGTTCAGCAGTTGCAGCAGGAAGACTT
 GGAGACCAAGCTGGAGAAAGGAATGGGGGTGTGCTGTTAACTCGCCGGAAGTCAGGGAGTCTTTGGGGGCCA
 GAAGTGTGGGACAGATTTTGGAAGAAGGAGAGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG
 CTGCAATGCCACACCTGTACCTGAAGCCGGACGCTGTGTGCGCATGGGCTGTGTGTGAAGACTGCCAGCT
 GAAGCTTCAGGAAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACTCCACAGAGTTCTGCAACAGGGCCAGCCC
 TCACTGCCAGCCTAATGTGTACTGTGCACAGTGGGCACTCATGTGAGGATGTGGACGCTACTGCTACAATGGCAT
 CTGCCAGACTCAGAGCAGCAGTGTGTCACTCTGGGGACAGGCTGCTAAACTGCCCTGGGATCTGCTTTGA
 GAGAGTCAATTCCTGAGGTGATCCTTATGGCACTGTGGCAAGTCTCGAAGAGTTCTTCTGCAAAATGGAGAT
 GAGAGATGCTAAATGTGAAAAATCCAGTGTCAAGGAGGTGCCAGCCGCCAGTCAATGGTACCAATGCCGTTTC
 CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTTCTGTGCCGGGGGACCCACGTTGACTTGGGCGATGA
 CATGCCGAGCCAGGCGTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA
 AAATATTAGTGTCTTGGGGTTCAAGTGTGCAATGCACTGCCAGGAGAGGAGTCCAGGCACTGTGCAAGAA
 CTGCCACTGCGAGGCCCACTGGGCACCTCCCTTCTGTGCAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGGCC
 CATCCGGCAAGCAGAGCAAGCGAGGAGTGCAGAGTCCAAAGGAGCGCGGCCAGGGCCAGGAGCCCGTGGG
 ATCGCAGAGCATCGCTCTACTGCTCACTGACACTCATTCAGGCCCTCCCATGACATGGAGACCGTGACCACTG
 CTGCTGCAGAGGAGGTCAAGCGTCCCCAAGGCCCTCTGTGACTGGCAGCACTGAGCTCTGTGGCTTGGCATCGTT
 TCCATGACACAGACACAAACAGTTCTCGGGCTCAGGAGGGAGTCCAGCTTACCAGGCACTGTGCAAGAA
 CAGTGCAGGAAGGGCAGCGACTTCTGTGTGAGCTTCTGTAAACATGGACATGCTTCACTGCTGCTCTCTGAG
 AGAGTAGCCAGTTACACTCTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGGAGCATCAAAAGTCTGGCCTTTC
 ACTGAGCTCCAGCAGTGGGGGAGAAGCAGGGTTTGGGCCAGTGTCCCTTTCCCGAGTGAACCTCAGCT
 TGGCAGCCCTGATGACTGGTCTCTGGCTCACTTAATGCTCTGATATGCTTTAGCATTTATATATGAAT
 AGCAGGGTTTTAGTTTTTAATTTATCAGAGACCTGCCACCCATTCATCTCCCAAGCAAACTGAATGGCAA
 TGAACAAACTGCAGAGAAGGTAGGAGAAGGCGGTGAATCTGTGCTCTTTGCTGTGGACATGGTGCAGGACG
 AGTACTCAGGTTTGGGGTTTGCAGAAAGCCAGGGAACCCAGAGTCAACCAACCTTCAATTTAACAAGTAAAGA
 TGTAAAAAGTGAACCAATGTAAGAGCTTAACCTCATCCCCGTGGCCATTACTGCATAAAATAGAGTGCACTT
 GAAAT

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09/09/2014 10:00

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><subunit 1 of 1, 735 aa, 1 stop
```

MAARPLFVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGLDWIPVKSFDISK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDSLARNYTGHCHYHGHVVRG
YSDSAVSLSTCSGLRGLIVFENESVYLEPMKSATNRYKLPKAKLKSVRGSCGSHHTPNLA
AKNVFPPPSQTWARRHKRETLLKATKYVELVIADNREFQQRQKDLKVKQRLEIETANHVDKF
YRPLNIRIVLVGVEVWNMDMKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFNMNHDTLDRGCSCQMAVEK
GGCIMNASTGYPPPMVFSSSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE
CDCGEPEECMNRCCNATTCTLKPDVAHAGLCCEDCQLKPAGTACRDSNSNCDLPEFCTGAS
PCHFANVYLHDHGSQCDVDGYCYNGICQTHEQQCVTLWVGPAGKAPAGICFERVNSAGDPYGN
GKGVSKSSFAKCEMRDCAKCKIKCQCGQSNRPIVGTNAGSIETNIPLQQGGRILCRGTHVYLG
DDMPDPLGLVLAQTCKADGKILCNRQCGQNI SVFGVHECAMQCHRGVCNNRNKNCHEAHWAPP
FCDKFGPGGSTDSGPIRQAEARQEAASERNRERGQGOEPVGSQEHASTASLTLLI

Signal peptide:

amino acids 1-28

FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA
ACAAAACAGTTTTTGGGGGTTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANITCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCCAGTGTCCTTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

09978375.101601

FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA
TTTCACCGTGTTAGCCAGGATTTGTCTCAATCTGACCTCATGATCTGCCCGCCTCGGCCTCCC
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAAACTTTTAAAGAAGTTAAT
GAAACCATACCTTTTACATTTTAAATGACAGGAAAATGCTCACAATAATGTTAACCCAAAA
TTCTGGATACAAAAGTACAATCTTTACTGTGTAATACATGTATATGTACTATATGAAAATA
TACCAAATATCAATAATACTTTATCTCTGGGTAAAAACCTCTTCTCATACCTCTGTCTAACAA
CTTTTAAACAAAAATTTGCATCACTTTTAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG
ACAGAAAAAAAACCAAGGGAAAAATCACGCCCACTTGGGAAAAAAGATTGGAATCTGCCT
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA
ACAAAGTACTTTGTCTGGATGTAGGAGGAAAGGAGTGATGTCACTGCCATTATGATGCCCC
TTGAATATAAGACCTTACTTGTCTATCTCCCTGCACAGCCAGGAGCCACCCATCCTCCAGC
ACACTGAGCAGCAAGCTGGACACAGGCACACTGATCCAATGGGTAAGGGGATGGTGCGA
TGCTCATTCTGGGTCTGCTACTTCTGGCGTGTCTCCTACCCGTGCAGGTTTCTTCAATTTGT
CCTTTAACCAGTATGCCGGAAGCTACTGCAGCCGAAACCAAAAGCCCTCCAACAGTGCCCT
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGTCTGCCCTTCTACATCTCTACCATTAAAGAGG
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAATGGTGCT
AGAAGTTCAATGTGGCAAGGAAAAAACAGGCTTTCATCAAACTCTACTAATTTCACTCCTT
ATTAAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT
GACTAGATGATAAATGCCTGTACTCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG
AGGTGAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA
AATATTGACTGGGCGTGGTGGTGAGTGCCTGTGATCCAGCTACTCAGGTGGCTGAAGCAGG
ACAATCACTTGAACCTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAGTGGCT
CACGCCCTGTAATCCCGGCACCTTTGGGAGGCCGAGGTGGGCGGATCACAGGTCAGGAGATCA
AGACCATCCTGGCTAATACAGTGAAACCTGTCTCTACTAAAAATACAAAAATTAGCCGGG
GATGGTGGCAGGCACCTGGAGTCCCAGCTACTCGGAGGCTGAGGCAGGAGAATAGCGTGAA
CTCAGGAGCGGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLIILGLLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL
LHLYH

Signal peptide:

amino acids 15-27

09978825.101601

FIGURE 34

GCCTGGCGAGAGCGCGCCAGCCCGCGCGGATGCCCCGCGGCCAGGACGCTCTCCCGCTGCTGGCCCGGC
 CGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCGGCATGGCGCGCGCGCGCGCTGGGGCGCCCGGGCCAGG
 AGCGCGCGCGCGCGCGCGCGCGGACGGGCCCGCCCGCGAGACGGCGAGGACGGACAGGACCGCGACAGCAGCACC
 TGTACACGGCGCGCATGTTTTCACGACGGGATCAGAGCGCGCGCGCACTTCTGTCATGTTCTTCGCGCCCTGGTGTG
 GACACTGCGCAGCGCTGCGACGGCACTTGAATGACCTGGGAGACAAATACACAGCATGGAAGATGCCAAAGTCT
 ATGTGGCTTAAAGTGAATGACCGGCCCACTCCGACGCTGTGCTCCGCCACAGGGGTGCGAGGATACCCCCACTTAA
 AGCTTTTCAAGCCAGGCGCAAGAAGCTGTGAAGTACCAGGGTCTCGGGACTTCCAGACACTGGAAAACTGGATGC
 TGCAGACACTGAACGAGGAGGCGAGTACACCCAGAGCGGAAAGTGGAAACCGCCCACTGCCCCGAGCTCAAGCAAG
 GGCTGTATAGGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAGGCGACCACTTTATCAAGTTCTTGGCTC
 CGTGGTGTGGTCACTGCAAGGCCCTGGCTCCAACTGGGAGCAGCTGGCTCTGGGCTTGAACATTCGAAACTG
 TCAAGATTGGCAAGGTTGATTGTATACAGCACTATGAACCTGCTCGGAAACCAAGGTTGGTGGCTATCCCACTC
 TTCTCTGGTTCCGAGATGGGAAAAAGTGGATCAGTACAAGGAAAGCGGGATTGGAGTCACTGAGGGAGTACG
 TGGAGTCGCGAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCAAGGCTTCAGAGGCCCGGTGCTGGCAG
 CTGAGCCCGAGGCTGACAGGGCACTGTGTTGGCACTCACTGAAATAAATCTCGATGACACCAATTCAGAGGAA
 TAACTTTCATCAAGTTTATGCTCCATGGTGTGGTCACTGTAAGACTCTGGCTCCTACTTGGGAGGAATCTCTA
 AAAAGGAATTCCTGGTCTGGCGGGGTCAAGATCGCCGAAGTAGACTGCACCTGCTGAACGGAATATCTGCAGCA
 AGTATTTCGGTACGAGGCTACCCCAAGTTATGCTTTTCGAGGAGGGAAGAAAGTCACTGAGCACAGTGGAGGCA
 GAGACCTTGACTCGTTACACCGCTTTGTCTGAGCCAAAGCGAAAGACGAACTTTAGGAACACAGTTGGAGGTGAC
 CTCTCTCGCCAGCTCCCGCACCTGCGTTTAGGAGTTCACTGCCACAGAGGCCACTGGGTTCAGTGGTGGCT
 GTTCAGAAAGCAGAACATACTAAGCGTGAAGTATCTTCTTTGTGTGTGTTTTCGAAGCAACACACTCTACAG
 ATTCTTTATTAAGTTAAGTTTCTTAAGTAAATGTGTAACCTCACTGGTCACTGTGTAAACATTTTCAGTGGCGATA
 TATCCCCCTTGACCTTCTCTTGATGAATTTATCACTGGTTTCCTTTGAGACTAAAATAGCTGTAGGGGAAATGAAA
 TTGCTGGACTTTTGGCTCTCTGAGTTGAGTGTATTTGGTGAAGAAAGCAGCATCCAAAGCATACTTTACTTGC
 CCAGGATTTCTGGAAGAGTGGCCCTGTGGCAGTATTGACCTTCTCTGATTTTAAAGTTCAGATTGACCTCAATAC
 TGTGTGTGCTCCGAGTACGAGCAGATGAAATGCAAAACCCACACTCTGAAGATACCTTCACGGCTGCGCTGC
 TGGAGCTCTGTTGCTGTGAATACTTCTCTAGTGTGAGAGGTAGCGGTGATGAAGACAGCGCTTACTTCTGACC
 GTGCTGAGTAAGAGAAAGCTGATGCTATACTTTATGTGTCGATACTTGTCAATCACTTACTGTTACGGGGAT
 CCTTCTGTTTCTCAGGGGTGAACATGCTTTAGTTCTCTATGTTAAACAGAAAGCAGAGGCCCACTGAAGCTGT
 TGGATGCTCTTCTTAGAAAGGATAGGCTAGGAAAATCCACGAGGCTCACTCTCAGTATCTCTAATCACTATTGA
 AAGATTCCAGTTGATTTGTGCACTCGGGGTGACAAAGACCAGACAGGCTTTCCAGGCTCGGTATCCAGGGAGGC
 TCTGCAGCCCTGCTGAAGGGCCCTTAAGTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCTTTTAGAGG
 CTGCTATACCTGCTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAAAGGATGAGTATGATCTCAAGAC
 CAAAGACAGATGTCAGTGGGCTGCTTGGCCCTGGTGTGACCGCTGTGGCAGCTGTGATGCCAGTGTCTCTA
 ACTCACTGCTGCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA
 GATAGGTGTTGTCTTTTACCATCGAGCTACTTCCATAATAAACCACTTTGCATCCAACTCTTCAACCCACCT
 CCCATACGCAAGGGGATGTGATACTTGGCCCAAAGTAACTGGTGTAGGAATCTTAGAAACAAAGACCACTTATA
 CTGCTGCTGAGGCGAAGATAACAGCAGCATCTGACCAAGCTTGGCTTAAAGGAAATCTTTATTAATCAG
 TATGGTTCAAGATAATCTTTTAAAAAAACCAACCTCTAGAGAAAGCAGCACTGTCAAGAGTCTGTACA
 CACAACCTCAGCTTGTGATCAGAGCTCTGTATCCAGAAATCAAGTGGTACAATTTGTTTGTACACTAT
 GATACTTTCTAAATAAATCTTTTAAAAA

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FIGURE 35

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLLPLLARPAALTALLLLLGHGGGGRWGARAQEAAAAADGPPAADGEDGQDPHS
KHLYTADMFTHQISAAHFVMFFAPWCCHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH
SDVCSAQGVVGYPTLKLKFKPGQEAVKYQGPRDFQTLENWMLQTLNEEPVTPEPEVEPPSAPE
LKQGLYELASNFELHVAQGDHFIKFFAPWCCHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHVELCSGNQVRGYPTLLWFRDGKKVDQYKGRDLESLEYYVESQLQRTETGATETVTPSEA
FVLAAEPEADKGTVLALTENNFDITIAEGITFIKFYAPWCCHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

Signal sequence:

amino acids 1-32

0978375.101601

FIGURE 36

CTTTTCTGAGGAACCAAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTGAGAGTCTGGGTCTGGATATTGATAGCCGCTCCTA
CCGCTGAAGTCTGTGCCACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAAATACCTGGAGAAAAAGGCAAAGCAGGTACT
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG
GGTGAATGCTAGCCATGCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTTTCGGGTGTTTCAATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA
TGTTCCACAGACAACACTCCACTGCAGAACTATAGCACTGGAATGAGGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT
ACGTATTGCTATTTTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTCCTG
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAA

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FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISFGPKGDDGEKGDGPGEEG
KHGKVGRMGPKGIKGEIGDMGDQGNIGKTGPIGKKGDGKEKGLLGIPGEKGKAGTVCDGGRY
RKFBVGQLDISIARLKTSMKFVKNVIAIGIRETEEFYIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYNSNWNEGEPSDPYGHEDC
VEMLSSGRWNDTECHLTMYFVCEFIKKKK

Signal peptide:

amino acids 1-25

0978375-101601

FIGURE 38

GGTTCTATCGATTTCGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC
 CCACGCGTCCGCTGCTCTCCGCCCGTGTGGAGTGGTGGGGGCTGGGTGGGAATGGGCGTGT
 GCCAGCGCAGCGCGCTCCCTGGAAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTT
 CGGAAGGGAGGATCAGGAGTGTTCGCGAGCGGCTGGAACCAAGCGGTGCCGATAGAGGAAGC
 GGGCTCCATTGGCTGCCCTCCTGCTGCTGCCCTGCTGCTGTGCTGCTGCTGCTGCTGCTGA
 AGCTACACCTCTGCGCCGAGTGTGCGCTGGCTTCGCGCGGACTTGGCCCTTTGCGGTGCGAGCT
 CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCCGGGCTGCCGCCGACCCGGAAGG
 TCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAATGGCCAGCAGCGCGCCGCGC
 ACACCTTTCTCATTACAGGCTCGCGCGCTTTAGCTACTCAGAGCGGAGCGCGAGAGTAAC
 AGGGCTGCACGCGCCTTCTACGTGCGCTAGGCTGGGACTGGGACCCGACGCGCGCGACAG
 CGGCGAGGGGAGCGCTGGAGAAGCGAGCGGGCAGCGCCGGAGACCGGAGATGCAGCGCGCG
 GAAGCGCGCGGAGTTTCCGAGGGGAGCGGTGCCGCCAGAGGTTGGAGGAGCCGCCGCCCT
 CTGTACCTGGAGCAACTGTGCGCTGCTCTCTCCCGCTGGCCAGAGTTTCTGTGGCTCTG
 GTTCGGGCTGGCCAAGGCCGCGCTGCGCACTGCTTTGTGCCACCGCCCTGCGCGGGGGC
 CCCTGCTGCACTGCCCTCCGAGCTGCGCGCGCGCGCGCTGGTGTCTGGCGCAGAGTTTCTG
 GAGTCCCTGGAGCCGACCTGCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG
 CCCAGGAACCCACCTGTCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG
 GGCCAGTGCCAGGATACCTCTCTTCCCCCAGAGCATAACAGACACGTGCTGTACATCTTC
 ACCTCTGGGACCAACGCGGCTCCCAAGGCTGCTCGGATCAGTCACTCTGAAGATCCTGCAATG
 CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCAC
 TCTACCACTGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGCGCACAGTG
 GTGCTGAATCAAAGTTCTCGGCTGGTCACTTCTGGGAAGATTGCCAGCAGCAGGGGTGAC
 GGTGTTCCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAAACAGCCCCGAGCAGAGGCAG
 AACGTGGCCATAAGGTCGGGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGGAGCGT
 TTTGTGCGGCGCTTCGGGCCCTGCAAGTGTGGAGACATATGGAAGTACAGAGGGCAACGT
 GGCCACCATCACTACACAGGACAGCGGGCGCTGTGGGGCGTGCTTCTGGCTTTACAAGC
 ATATCTTCCCTTCTCCTTGATTGCTATGATGTACCAACAGGAGGCCAATTCCGGGACCCC
 CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCGGTGAAGCA
 GCAGTCCCCATTTCTGGGCTATGCTGGCGGGCAGAGCTGGCCAGGCGCTCTGTCTAAAGG
 ATGTCTTCCGCGCTGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA
 GGTTTTCTCCGCTTCCATGATCGTACTGAGACACCTTCAGGTGGAAGGGGAGAAATGTGGC
 CACAACCGAGGTGGCAGAGGCTTCGAGGCCCTAGATTTTCTCAGGAGGTGAACGCTCTATG
 GAGTCACTGTGCCAGGTCATGAAGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC
 CACGCTTTGGACCTTATGTCAGCTCTACCCACGCTGTCTGAGAATTTGCCACCTTATGCCCG
 GCCCCGATTCTCAGGCTCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG
 TTCGATGGCAAAATGAGGGCTTCGACCCAGCACCTGTCTGACCACTGTACGTTCTGGAC
 CAGGCTGTAGGTGCCCTACCTGCCCTCACAACCTGCCCGGTACAGCGCCCTCTGGCAGGAAA
 CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGTGGGGG
 CCGTTGCAGGTGTCTGGGCTGTGAGGATCTTTCTATACCAAGACTGCGGTCACTATTTT
 GTAATAAATGTGGCTGAGCTGATCCAGCTGTCTCTGACCTAAAAAAGAAAAA
 AAAAAAAGGGCGCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC
 TTGGCCGCATGGCCCACTTGTATTATGACG

0978375.101604

FIGURE 39

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913

><subunit 1 of 1, 730 aa, 1 stop

><MW: 78644, pI: 7.65, NX(S/T): 2

MGVCQRTAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLPLLLLLPL
LLLKLHLWPLRLPADLAFVRLALCKKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ
RAAHTFLIHGSRFRFSYSEAEERESNRAARAFRLALGWDWGPDDGDSGEGSAGEGERAAPGAGD
AAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRTAFVPTAL
RRGPLLHLCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGPVPGYLLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLGIVGCMGIGATVVLSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP
SKAERGHKVRILAVGSGRLRPTDWERFVRRFGPLQVLETYGLTEGNVATINITYTGQAGVGRASW
LYKHIFPFSLIRYDVTGTGEPIRDPQGHCMATSPGEPGLLVAPVSSQSPFLGYAGGPPELAQGGK
LLKDVFRPGDVFFNTGDLVCDQGFRLRFHRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site
starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain signature

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCAACACATACCTCCACGCACA
 CACATCCCCAAGAACCCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTC
 GCTTGTTCACATCTCCCTCCGGGGGAGCCGGCGCGCTCCACCTTTGGCCGACACTCCGGC
 GAGCGCAGCCCGACGCTCCAGGATTCTGCGGCTCGGAACCTCGGATTGACAGTCTGAAACC
 CCATGGTGGTTTTTTAAACACTTCTTTTCTCTCTTCTCGTTTGTATGACCGTTTTCCA
 TCTGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTGTGCTTGCCATCGT
 CCATCTGGCTTATAAAAGTTTGTCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCCTCGG
 CTGGCAGAAGGGGGTGACGCTGGGCAGCGCGAGGAGCGCGCGCTGCTCTGGCGGGCTTT
 CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCGGTGGGGTTTACCAGCTGGATTGTATG
 TTGCACCATGCCCTTCTTGGATCGGGGCTGTGATTCTTCCCTCTTGGGGCTGCTGCTCTCCC
 TCCCCCGGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCGCCAGGCGTACGGTGCC
 AAGGGATTACGCTTGGCGGACATCCCTACCAAGGAGATCGCAGGGGAACACTTAAAGAACTGT
 TCTTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAGTTAAGCCAACAAGCAAAAC
 TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG
 CATAAGAAATTTGACGAATTTTCCGAGAGCTCCTGGGAATGCAGAAAAGTCACTAAATGA
 TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTGAGAAGTCTTCCAGGACCTCT
 TCACAGAGCTGAAAAGGTACTACACTGGGGTAAATGTGAATCTGGAGGAATGCTCAATGAC
 TTTTGGGCTCGGCTCCTGGAACGGATGTTTACGCTGATAAACCTCAGTATCACTTCAGTGA
 AGACTACCTGGAATGTGTGAGCAAATACACTGACAGCTCAAGCCATTGGAGACGTGCCCC
 GGAAACTGAAGATTACGTTTACCCGCGCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG
 ACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTCAGCCCAACCCAGGTTGTATCCG
 TGCCCTCATGAAGATGCTGTACTGCCCATACTGTGCGGGGCTTCCCCTGTGAGGCCCTGCA
 ACAACTACTGTCTCAACGTCATGAAGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG
 TGGAACTCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT
 TGAGTCGGTTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA
 ACAGCATGCAGGTGTCTGCAAAGGTCCTTTCAGGGATGTGGTCAGCCCCAACCTGCTCCAGCC
 CTCAGATCTGCCGCTCAGCTCCTGAAAATTTTAATACAGTTTTCAGGCCCTACAATCCTGA
 GGAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA
 AATTGAAGCTCTCTAAAAGGTCGTGGTCAGCATTACCTACATATCTGCAAGGACGAGAGC
 GTGACAGCGGCACGTTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACCTT
 GCCTGAGATCATGAATGATGGGCTCACCAACAGATCAACAATCCCGAGGTGGATGTGGACA
 TCACCTCGGCTGACACTTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA
 CTAAAAACGCTTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG
 CTCAGGGAGTGGCAGTGGGTGCAATGGATGACGTGTGCCACGGAGTTTGTAGTTTGTACCA
 CAGAGGCCCGCAGTGGATCCGACCGGAGAGAGGTGGACTCTTCTGCAGGCCAGCGTGGC
 CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCTTGGCAGTGCAGAGACTGTGCAGATA
ATCTTGGGTTTTTGGTCAGATGAAACTGCATTTTAGCTATCTGATGGCCAACCTCACTCTT
 TTCTTACACTCTTGGACAATGGACCATGCCACAAAACCTTACCGTTTTCTATGAGAAGAGAG
 CAGTAAATGCAATCTGCTCCCTTTTGTCTTCCAAAGAGTACCGGGTGGCAGACTGAACTG
 CTCTCTCTTCTTCTTACGCTATCTGTGGGACCTGTTTATTTCTAGAGAGAACTTCTACTCAA
 ATTTTTCTGACCAGGAGATTTTCTTACCTTCATTGCTTTTATGCTGCAGAAGTAAAGGAAT
 CTCAGTTGTGAGGGTTTTTTTTTCTCATTAAAAAT

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FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADVKA RSCGEVRQAYGAKGFS LADIPYQETIAGEHLRICPQ
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFRELL ENAEKSLNDMF
VRTYGMLYMQNSEVFQDLFTELKRYYTGGNVNLEEMLNDFWARLLERM FQLINPQYHFSEY
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSP TPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDT EWNLFIDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMNMQENSMQVSAKFQCGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDES VTAGTSNEEECWNGH SKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDVDCPTEFEFVTT EAPAVDPDRREVDSSAAQRGHSLLSWSLT CIVLALQRLCR

Signal peptide:

amino acids 1-23

09/03/95 10:00:01

FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAAACGCACG
 CAGTTTTCAGCGCCTGCGCGCGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGG
 TAGGGACCCGGCTTTGGCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATGTCTGCCGGAGTTTCTGCGGAGGT
 GGAGGGAGATCAGGAAACGGCTTCTCTCTCACTTCGCGCGCTGGTGAAGTGTCTGGGGAGATTTGGCAAACGCATTAGG
 AAAGGACTGGGGAAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTATCTG
 TCTGATCAGAGCCAGACGCGAGCGCTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGCGCGA
 TCCGCCGCCCTCCGTACCAACGACTCCAGGAGAGTCAGCCTCGCTCCCCAACGTCGAGGGCGCTCTGGCCACGA
 AAAGTTCTCGTCCAGCTGTGATTCTCAATTCTTGCTTGGTTTTTTCTCCAGAGAACTTTGGGTGGAGATATTA
 ACTTTTTCTTTTTTTTTCTTGGTGAAGTCTCTAGGAGGGGGGAGGAGGAGGAGAAAGTGAATGTGC
 TGGAGAGAGCGAGCCCTCTTGTCTTCGCGAGTCCATCCATTAAAGCCATCACTTCTGGAAGATTAAAGTTGT
 CGGACATGTTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTACCGTCTGTTGGGTGCATG
 TGTGCGCCGACGCGCGCGGGCGGTGGTTCTCCGCGTGAAGTCTCACTGGGACCTGAGTGAATGGCTCCCA
 GGGGCTGTGCGGGGCAATCGCTCCGCTTCGCCACAGGCTGTGTCTGCTCTGGAAGATGCTAGCAATGGGG
 CGCTGGCAGGATCTCGATCCTTCGCTCCTCACTTTATGGTTACCTGTCTGGGGCCAGGCTTAGAAGAGGAGG
 AAGAGGGGCCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACTTCACCTCCAGCCCCATCTCA
 TTTTCATCTAGCGGATGATCAGGATTTAGAGATGTGGGTACCACGGATCTGAGATTAACCAACCTACTCTTG
 ACAAGCTCGCTGCCGAGGAGTTAACTGGAGAATCTACTATGTCCAGCCTATTGACACACCATCCAGGAGTCAGT
 TTATTACTGGAAGTATCAGATACACACCGGACTTCAACATCTATCATAAGACCTACCCAAACCAACTGTTTAC
 CTCTGGAATGCCACCTACCTCAGAACTGAAGAGGTTGGATATTCAACGCATATGGTTCGGAAGTGGCACT
 TGGGTTTTTAAAGAAAGATGATGCCACAGAGAGGATTTGATACCTTTTTTGGTTCCTTTTGGGAAGTG
 GGGATTACTATACACTACAAATGTGACAGTCTTGGGATGTGTGGCTATGATTTGATGAAAACGACATGCTG
 CTTGGGACTATGACAAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCCAT
 ACCCCACAAAGCTATATTTTTATATATAGCCTATCAAGCTGTTTCACTTACCACCTGCAAGCTCCTGGCAGGTATT
 TCGAACACTACCGATCCATTATCAACATAAAGAGGAGATATGCTGCCATGCTTTCTGCTTAGATGAAGCAA
 TCAACAAAGTGAATGGCTCTAAAGACTTATGGTTTCTATAAACAAGCATTTATCATTTACTCTTCAGATAATG
 GTGCCAGCTTACGGCAGGAGGAGTAACTGGCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGATCC
 GGGCTGTAGGCTTTGTGATAGCCCACTTCTGAAAAACAAGGAAACAGTGTGAAGGAACCTGTGCACATCACTG
 ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTTGATGAGGACATTCAACTAGATGGCTATGATATCT
 GGGAGACCATAAGTGAGGGTCTTCGCTCACCCGAGTAGATATTTTGATACAAATTGACCCCTATACCAAGGC
 AAAAAATGGCTCTGGGACAGGCTATGGGATCTGGAACATGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
 GAAATGTCTTACAGGAAATCCTGGCTACAGCGATGGGTCCCCCTCAGTCTTTTTCAGCAACCTGGGACCGAACCG
 GTGGCACAATGAACGATCACTTTGTCACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA
 GAGGGTGGACCTATCTAAAGGTATCTCAGGAATCTGTAAGAAGCTCTACGAGGCTCTCAGAGTTCAACAAAC
 TGCAGTGCCGCTCAGGTATCCCCCAAAGACCCAGAAGTAACCCTAGGCTCAATGGAGGGGTCTGGGAGCCATG
 GTATAAAGAGGAACCAAGAAAAGAGCCAAAGCAAAATCAGGCTGAGAAAAGCAAAAGAAAAGCAAAAAA
 GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACAGCAAAATTTGGCTCGATAATATCGCTGGCCCTAAGCGTCA
 GGCTTGTCTTCTGCTGTGCCACTCAGAGACTTCTGCCACTTGGCCGCCACACTGAAACTGTCTGCTCAGTG
 CCAAGGTGCTACTCTTTCAGGCCACACTTAGAGAGAGTGAGATGTTTATTTCTCTGCTCCTTTAGAAAACGCTG
 TGAGTCTGAGTTTCACTGCTGTGCTTCACTCAACTGACCAAAACACTGCTTTGAATTAAGGAGGAGAAACATA
 ACCTACCTCGCAAGTGTCTAATTTGATGGAAGTTACAGGGTAGCATGATTAACAACTACCTTTGATAAATTAC

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FIGURE 42B

AGTCAAAGATTGTGTACCTCAAAGGCCTTGAAGAATATATTTCTTGGTGAATTTTGTATGTCTGTCATATGA
CACTTGGGTTTTTTAATTAAATTCATTTTATATATATAAATATATGTTCTTCTTCTGTGAAAGCTGTTTTTCT
CACATGTGAACAGCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCC
ACAATGAATGTAACATTTTCTAAACCTTTACTAGAAGAACATTTTCAGTATAAAAAACCTAATTTATTTTACA
GAAAAATATTTTGTGTTTTTATAAAAAAGTTATGCAAATGACTTTTATTTTATTTCTGTGCATACCATTAGAAGA
ATTTTATTTTCATTTCTTCAAATTATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTGAGACTA
TAAAAAACATCATTGAGAAAACCTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT
ATTACTTGGAAATTCATGTTTTGTGCAGAGTTGAGACAACCTTTATGTTTCTATCATAAATCTTTATGTTATCTT
AATTATTAATGATTTACTTTATGGCACTAGAAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAAAT
GTATCATTTGGTCTTAAAAATAAAAAATCTTTACTAATAGGCAATGAAGGAATGGTTTGTGTAACAACCAAGTAA
TATAATATGATTTTACAGATAGATGCTTCCCTTGGCTATGACATGGAGAAAGATTTTCCCAATAATAAATACTAA
TATTTATATTAGGTTGGTGCAAACTAGTTGCGGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAAAGT
GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCTGGAGTAGGTAACCTTGCTTGGAAACCCC
ACATGCAAACTGATGAGGAGAAATTAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTGATCAATGAGCATA
GATTGGTGTGGATCCTGTAGACCTGGTGTCTTTCTTGAAGTGCCCTCTCCTAATGCAGAGGCCCTTGAAGCTTAC
AGTATACACTTGAAGTCAAGATAGCTAGAAATATGATCTTTGAAGTTATAACTGTGATCTGAAAAATGTGTGT
GGTGGTATGACAGCATAACATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTATATCAC
AACTCAAAGGACTGTGATATAATCCATTATATCACAGCTCACAGTTTCTGAAAAATGATAAAGAATCTATAAT
CTAGTACTGAAATTACTAAATGGGTAAGATGATTTAAATGATTTTAAATTTAATTTTAACTTTTATTTCTAGAAATAT
GGCTCCATTTTATTTATAGTGTAAGTTGATTTCTTAAAGTTTGTGTTTTGTCGACAGATCTTTTAAATGAG
TCTTAAAAATAAAGGCATATTGTTTCATGTTTAAA
AAA

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FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEEEGALLAQA
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYPHGSEIKTPTLDKLAABGVKLENYVQPICTP
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGVGNHLGFRKEC
MPTRRGFDFTFFGSSLLGSGDYTHYKCDSPGMCYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAYQAVHSPQAPGRYFEHYRSIININRRRYAAMLSCLDEAINNVTLA
LKTYGFYNNSSIIYSSDNGGQPTAGGSNWPLRGSKGTWEGGIRAVGFVHSPLLKNKGTVCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQPSECSGTGNCLQEILATATGSPLSLSATWDRGTGGTMNGSPCQLAKVYGFS
TSQPTHMRGWTYLTGIQES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

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FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGCT
TTAGCTGCTACGGGGTCCGGCCGGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCCAGAAATGCCCTCTGCCCTGGAGCCCTTGCGCTCCCGCTGCTGCTCTCCTGGGTGGCAG
GTGGTTTCGGGAACCGGCCAGTGC AAGGCATCAGCGGTTGT TAGCATCGGCACGTCAGCCT
GGGGTCTGTCACTATGGAACATAAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCCTGGGACCAAAACAAAT
GCAGATGCTTTCCAGGATACACCGGGAAAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGTCTTTGCCCT
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTTAGGACATGTGCCATGATAA
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA
CTCCGCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAATGTCACA
TTGGTTTCGAACATGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGTCCTTCAAGTG
TAAATGCAAGCAGGATATAAAGGCCAATGGACTTCGGTGTTCTGCTATCCCTGAAAATTTCTG
TGAAGGAAGTCTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
AAAAACAGCATGAAAAAGAAGGCCAAAAATTAAAAATGTTACCCAGAACCCACCAGGACTCC
TACCCCTAAGGTGAACCTTGCGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAACT
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAAGAGGGGCTTGAGGATGAGAAAAGAG
AAGAGAAAGCCTGAAGATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTCCCT
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA
ACTGGAACATAAAGATTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT
GGAAACAGGATAGAGAAGATGATTTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC
TTCTATATGGCAGTTCCGGCCTTGGCAGGTCAAGAAGACATATGGCCGATTGAAACTTCT
CTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG
ACAAAGTCGGGAAACTTCGAGTGTGTTGTGAAAAACAGTAACATGCCCTGGCATGGGAGAAG
ACCACGAGTGAGGATGAAAAGTGAAGACAGGGAAAAATTCAGTTGTATCAAGGAACATGATGC
TACCAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAACCGGCAGAAATCGCAGTGG
ATGGCGTCTTGCTTGTTCAGGCCTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG
TTACTATCTTTATATTGACTTTGTATGTGAGTTCCCTGGTTTGTGATATTGCATCATAG
GACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAAAATTATTG
TAAGATGCCCTTTCTGTATAAGATATGCCAATATTGCTTTAAATATCATATCACTGTATCT
TCTCAGTCATTTCTGAATCTTCCNCATTATATTATAAAATNTGGAANGTGAGTTTATCTC
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTCTA
GAAAATAGAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTCTTGA
AACTATGACATCAAAGATAGACTTTTGCCCTAAGTGGCTTAGCTGGTCTTTCATAGCCAAAC
TTGTATATTTAATTCTTTGTAATAATAA

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Signal peptide:

EGF-like domain cysteine pattern signature.

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGCTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCCC
AGAAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG
AGCTGGCTTACAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTCAGCCAGAAGAGTGCAT
GAGCTGGAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT
TGTTTTGCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAAATGTCCAGCGTTCTCTGTGC
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTCT
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCATTGGATACTGTGCTAGCAAGCATGCT
CTCGGGGTTTTTTAAATGGCCTTCGAACAGAAGTGGCACATACCCAGGTATAATAGTTTC
TAACATTTGCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCTAGCTGGAGAAGTCA
CAAAGACTATAGGCAATAATGGAGACCAAGTCCACACAAGATGACAACCAAGTCGTTGTGTGCGG
CTGATGTTAATCAGCATGGCCAATGATTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAATC
TTTAAGACAAAACATGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT
ACTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAATAAATAATAAAAG
ATTGCCATGAATCTTGCAAAA

[illegible]

Important Features:

amino acids 1-31

amino acids 136-157

106-113 and 107-114

amino acids 80-90, 131-168, 1-13 and 176-185

FIGURE 48

GCGACGTGGGACACGCCATCAGCTGTTTCGCGCTCTTCTCCTCCAGGTGGGGCAGGGGTTT
 GGGCTGTTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTCCG
 TTGCATCTTCTACACACTACAGCTATGTGTTAGGTTGCTGCGGACACGCTGGGCCTCTGTCC
TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGGCTGGATCCTGTTT
 TTCGTGCTTATGATTTCTGCATTGTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT
 GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCATGAGCCCTCA
 ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG
 GACAGCGTGGCCCCGGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC
 TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC
 CTGGGTCTCACTGCTGCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCTGTGT
 CAGTGGTCTCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
 GCTGCCCTGCAGTTGCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGTG
 GCAGCTCGCCACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC
 CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCACTGATGCTCTCTGGGACC
 CTACGCAATCTGCGCCTGCGTCTCATCAGTGCGCCACATGTAACGTATCTACAACAGCT
 GCACCAGCGACACCTGTCCAACCCGGCCCGGCTGGGATGCTATGTGGGGGCCCCAGCCTG
 GGGTGCAGGGCCCCCTGTCAAGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA
 CACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGT
 GCTGCTGACCAACACAGCTGCTCACAGTTCTTGCTGCAGGCTCGAGTTTCAGGGGGCAGCTT
 TCCTGGCCAGAGCCAGAGACCCCGAGATGAGTGTGATGAGGACAGCTGTGTAGCCTGTGGA
 TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCT
 GATGCACCAGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTG
 CTGCCACTGCTTCATTGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACAGA
 CCGGAGGAGTGGGGCTTGAAGCAGCTCATCTGCATGGAGCCTACACCCACCTGAGGGGG
 CTACGACATGGCCCTCCTGTGCTGGCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC
 TCTGCTGCCCTATCTGTACCACCACCTGCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG
 GCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCTGGGGCCCTAG
 GGCTGCGAGCCGGCTGCATGCGCTCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG
 TGTGTACCAGTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCCTGTCTGGGGCAACCATGGTG
 CATGAGGTGAGGGGCACATGGTTCTTGCCGGGCTGCACAGCTTCGGAGATGCTTGCACAGG
 CCCCGCCAGGCCGGCGGTCTTACCGCGCTCCCTGCTATGAGGACTGGGTGAGCAGTTTGG
 ACTGGCAGGTCTACTTCGCGGAGGAACAGAGCCGAGGCTGAGCCTGGAAGCTGCCTGGCC
 AACATAAGCCAACCAACAGCTGCTGA CAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC
 AGGCAGGCAAAATGGCATTACTGCCCTGTCTCTCCACCCCTGTCATGTGTGATTCCAGGCAC
 CAGGGCAGGCCCAGAAGCCAGCAGCTGTGGGAAGGAACCTGCTGGGGCCACAGGTGCCCA
 CTCCACCCCTGCAGGACAGGGGTGCTGTGGACACTCCACACCCAACTCTGCTACCAAGC
 AGGCGTCTCAGCTTCTCTCTCTTACTCTTTAGATACAATCAGCCAGCCAGCTGTTT
 TGAAAATTCTTTTGGGGGGCAGCAGTTTCTTTTAAACTTAAATAAATTGTTTAC
 AAAATAAAA

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FIGURE 49

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSSLVSLAGSVYLAWILFFVLYDFCIVCITYAINVSLMWLSFRKVQEPQGKAKRHGNTV
PGEWFPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDLALLQLAHPHTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRLRLRLISRPTCNCIYNQLHQRHLSNPARGMLCGGPQPGVQGPCQGDSGGFVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQGLACGALVSEEAULTAAHCFIGRQAPPEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERG
WVLGRARPGAGISSLQTVPVTLTGPRACSRLLHAAPGGDGSFILPGMVCTSAVGELPSCGELS
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPE
GSCLANISQPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family

amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

FIGURE 50

CGGGCCGCCCCCGCCCCCATTCGGGCCGGGCCTCGCTCGCGCGGCGACTGAGCCAGGCTGG
GCCGCGTCCCTGAGTCCCAGAGTCGCGCGGGCGCGCAGGGGCAGCCTTCCACCACGCGGAG
CCCAGCTGTGACGCGCCTCACAGGAAGATGCTGCGTCGGCGGGGAGCCCTGGCATGGGTGT
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCAGG
TCCTTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGTCTCTCTCTCC
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGCAGAGATACCAACA
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCTATGCCAACCGCACGGCCC
TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCCTGTGGCG
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTTCGGCAGCGCTGCCGTGAGCCT
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCTTGAGGCCAACAAAGGACCTGCGGC
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCTTGAGGCTGAGGTGTTTC
TGGCAGGATGGGCAGGGTGTGCCCTGACTGGCAACGTGACCACGTCGCAGATGGCCAAACGA
GCAGGGCTTGTTTGATGTGCACAGCGTCTCGCGGGTGGTGTGGGTGCGAATGGCACCTACA
GCTGCCTGGTGCAGAACCCCGTGTGCAGCAGGATGCGCACRGCTCTGTCAACATCACAGGG
CAGCCTATGACATTTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGTGTGTGTCTGTCTCAT
TGCACTGCTGGTGGCCCTGGCTTTCTGTGTCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTTGACCATGAGGACCAGG
GAGCTGTACCCCTCCCTACAGCTCCTACCTCTGGCTGCAATGGGGCTGCAGTGTGAGCCC
TGCCCCCAACAGATGCATCTGTCTGACAGGTGGGCTCCTTCTCCAAGGATGCGATACAC
AGACCACGTGCAGCCTTATTTCTCCAATGGACATGATTCCTCAAGTCATCCTGTGCCTTTT
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCCTC
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTGAGA
CTGACTGACCCCTGCCTTATTTTACCAAAGACAGATGCATAGTCACCCGCGCCTTGTTTC
TCCAATGGCCGTGATACACTAGTGATCATGTTGAGCCCTGCTTCCACCTGCATAGAATCTTT
CTTCTCAGACAGGACAGTGCAGGCTCAACATCTCCTGGAGCTAGAAGCTGTTTCCCTTTC
CCCTCCTTCTCCCTGCCCCAAGTGAAGACAGGGCAGGGCAAGGAATGCTTTGGGGACACCG
AGGGGACTGCCCCCCACCCCAACCATGGTGTATTCTGGGGCTGGGGCAGTCTTTTCTGGC
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG
GATGTCTATCTCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC
TCGGAGGGATTTTGTAACTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAA
AAAAAAAAAAAAA

09978375.101601

FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTATLCCSFSPEPGFSLAQ
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQVRVVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTTITCSSYQGYPEAEVFWQDQGQVPL
TGNVTTSQMANEQGLFDVHSLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTPFPEA
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEENAGAEDQDGEGEKSTALQPLKHSDSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

0978375-101604

FIGURE 52

TTCGTGACCCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC
 CTGAACCTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG
 AGGGACCTTTCCGCTGTCTTTTGTAGGGACTTCTTTCTTGTCTCAGCAACATGAGGCTTTTCT
 TGTGGAAACGCGGTCTTGACTCTGTTTCGTCACTTCTTTGATTGGGGCTTTGATCCCTGAAACCA
 GAAGTGAATAATTGAAGTTCTCCAGAAGCCATTATCTGCCATCGCAAGACCAAAGGAGGGGA
 TTTGATGTTGGTCCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTTATTTCACTCCACTC
 ACAAACATAACAAATGGTCAGCCCCATTTGGTTTACCCTGGGCATCCCTGGAGGCTCTCAAAGGT
 TGGGACCAAGGGCTTGAAGGAATGTGTGTAGGAGAGAAGAGAAGCTCATCATTTCTCTCTGC
 TCTGGGCTATGGAAAAGAAGGAAAAGGTAAATTTCCCCAGAAAGTACACTGATATTTAATA
 TTGATCTCCTGGAGATTTCGAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT
 AATGATGACTGGAAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA
 ACATGGTGGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAG
 AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA
 TAGAGATACATCTACCCCTTTTAAATATAGCACTCATCTTTCAAGAGAGGGCGAGTCATCTTAA
 AGAACATTTTATTTTTATACAATGTTCTTTCTTGCTTTGTTTTTATTTTTATATATTTTTT
 CTGACTCCTATTTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT
 GGGAAAGAAAAGCTAATTGGTCTTTGAATAGAAGACTCTCGGACAAATTTTTCACTTTCACAG
 ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC
 ACGACATGAGACCAGGTATAGCACAAATTAGCACCCCTATATTCTGCTTCCCTCTATTTTC
 TCCAAGTTAGAGGTCAACATTTGAAAAGCCCTTTGCAATAGCCCAAGGCTTGCTATTTTCAT
 GTTATAATGAAATAGTTTATGTGTAACCTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA
 TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG
 TTAGAAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCTGTAAATCCAGCACTTTGGGAG
 GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACCGGAGAAAA
 CCCTATCTCTACTAAAAATACAAAGTAGCCCGCGTGGTGTATGCGTGCTGTAATCCAGCT
 ACCCAGGAAGGCTGAGGCGGCAGAAATCACTTGAACCCGAGGCGGAGGTTGCGGTAAGCCGAG
 ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACACGGTTAATACCATATNA
 ATATGTATGCAATTGAGACATGCTACCTAGGACTTAAAGCTGATGAAGCTTTGGCTCCTAGTGAT
 TGGTGGCCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAAATAAATG
 TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC
 TAGCGGAATATCCTTCTGTGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA
 TTGTATCATAAAGATAAAGTAGTAAACAGTCTACATTTTCCATTTCTGTCTCATCAAAAAC
 TGAAGTTAGCTGGGTGTGGTGGCTCATGCTGTAATCCAGCACTTTGGGGGCCAAGGAGGG
 TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCCAACATGGTGAAACCTTGTCTCTA
 CTAAAAAATACAAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCAGCTACTCGGGAG
 GCTGAGACAGGAGATTGCTTGAACCCGGGAGGCGGAGGTGCAAGTGAGCCAAAGATTGTGCC
 ACTGCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGAGCAGA
 CCTACAGCAGCTACTATTGAATAAATACCTATCTGAGATTTT

09976375.101601

FIGURE 53

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194
><subunit 1 of 1, 211 aa, 1 stop
><MW: 24172, pI: 5.99, NX(S/T): 1
MRLFLWNAVLTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSL
FHSTHKHNNQQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLKDEVKAYLKKEFEKHGAVVNESHHDALVED
IFDKEDDKDGFISAREFTYKHDEL

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

00978375-101501

FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTAGCAT
 CCAACCATTCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCCTCTCCCGTAGCCCCACCGA
 CTAACATCTCAGTCTCTGAAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT
 CACGGGGCTCAGTCTCTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC
 CTGCCACCCTCAACGTCTCAATGGCTCTGACGCCCGCCTGCCCTGCACCTTCAACTCCTGC
 TACACAGTGAACCAACAAACAGTTCTCCCTGAATGGACTTACCAGGAGTGCAACAACAGTCTC
 TGAGGAGATGTTCTTCCAGTTCCGCATGAAGATCATTAACTGAAAGCTGGAGCGGTTTTCAAG
 ACCCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTG
 CAGCCGGAGGATGAGGGGATTTACAACGTCTACATCATGAACCCCCCTGACCGCCACCGTG
 CCATGGCAAGATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG
 CCGTGATGTGGGGTGCTCCGTGCGGGGCTTCCCTGGCTGTGGTCACTCTTGGTGCTGATGGTG
 GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA
 GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTGTGGGTGGCGGGC
 CTGCAGCCTCCCGTGTCCGTCTCCTCCCTCTCCGCCCTGTACAGTGACCTTGCTGTCTG
 CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCACCTGGGGCCTCCTGAAACCCCG
 ACTTCGTATCTCCCACCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA
 TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCCACCTGCCAGTCCCTGG
 GGGGAGGCAGGAGGCACATGTGAGGGTCCCAGAGAGAAAGGGAGTGGGTGGGCAGGGGTAGA
 GGAGGGGCGCTGTACACTGCCAGTGCTTGCCTGGCAGTGGCTTACAGAGAGACCTGGTGG
 GGAGGGAGGGCTTCTCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG
 TGCTCCTCCCTGCTCCCAGCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA
 AACTTGGAGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCAGTGACGGAAGCCAGGG
 CTGCAGGCAAGCTGGACATGTGCCCTGGCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT
 GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG
 ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCCAGCGGGACCCACCAACAGAGGCC
 AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAG
 GCTCTGCCTTCTCCATGGGGTAACCAACCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT
 GAGGAGGCCATGCACAGGGTGGGGCAGCTTCTTTGGGGCTTCACTGAGAACTCTCCAGTT
 GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAGCCTGAGGCCG
 GCATAAGGGGAGGCCTTGAACCTGAGCTGCCAATGCCAGCCCTGTCCATCTGCGGCCACG
 CTACTCGCTCCTCTCCAAACAACTCCCTTCGTGGGGACAAAAGTGACAATTTAGGCCAGGC
 ACAGTGCTCAGCGCTGTAATCCAGCACTTTGGGAGGCCAAGCGGGTGGATTACCTCCAT
 CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG
 GTGGCGTGTGCTGTAATCCAGCTATTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG
 GGAAGCAGAGGTTGCAGTGAACCTGAGATAGTATGATGCCACTGCAATTCAGCCTGGGTGAC
 ATAGAGAGACTCCATCTCAAAAAA

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005083 101603

<subunit 1 of 1, 215 aa, 1 stop

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATNLVLNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLRFQDRVEFSGNPSKYDVSVMRLRVQPEDEGI
YNCYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAIVGASVGGFLAVVILVLMVVKCVRRK
KEOKLSTDDLKTEEEGKTGEGNPPDGA

Signal peptide:

amino acids 1-20

amino acids 161-179

amino acids 83-127

amino acids 42-45, 66-69 and 74-77

FIGURE 56

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCCGCCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAACCTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG
TTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
GAACCCAGCAAGTACGATGTGTTCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAACCTGCTACATCATGAACCCCCC

09978375.101601

FIGURE 57

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTNCACATA
CCTGCCACCCCTCAACGTCCTCAATGGCTTTGACGCCCCGCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTCCGTGATGC
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCC

0978375.101601

FIGURE 58

TGCGGCGACGCGTGTACACCAATGGGCGCTCCACCTCCGCCCCCTACCGTGTGGGGCTGCTCCGCGATGGCCCTCTGT
 TCCTCTTGTGCTGCTAATGCTGCTTCGCGGACCCAGCGCTCCGCGCGGAGCTCACCCCCAGTGGTGTGCTGCTCC
 CTGGTGAATTGGGTAAACCACTGCGGAAGCCAGCTGGACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAAGAAGA
 CCGAAGCTACTTCACAATCTGGCTGACACCTGGAACTGCTGCTGCTGCTATCATATGACTGCTGGATTGACAAATA
 TCAGGCTGGTTTACAAACAAACATCCAGGGCCACCCAGTTTCTGATGGTGTGGATGTACGTGTCCCTGGCTTTG
 GGAAGACCTTCTCACTGGAGTTCTCGGAGCCAGCAAAGCAGCGTGGGTTCCTATTTCCACACCATGGTGGAGA
 GCCTTTGTGGGCTGGGGCTACACACGGGCTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCGAGCCCAAATG
 AAAACGGGCGCTACTTCTGGCCCTCCGCGAGATGATCGAGGAGATGTACAGCTGTATGGGGGGCCCGCTGGTG
 TGGTTGCCACAGTATGGGCAACATGTACAOGCTCTACTTTTGCAGCGGCGAGCCGAGGCTTGGAAAGGACAAGT
 ATATCCGGGCGCTTGTGTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAGACCCCTGCGGCTCTGGCTTCAGGAG
 ACAACAACCGGATCCAGCTCATCGGGGCCCTGAAGATCCGGGAGCAGCAGCGGTGCTGTCCACAGCTGGC
 TGCTGCCCTACAACTACACATGTGTCACTGAGAAGGTGTTCTGTCAGACACCCACAATCAACTACACACTGCGGG
 ACTACCGCAAGTTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGG
 AAGCCAGATGCCACTGGCGTGCAGCTGCCTCTATGGTACTGGGCTCCCCACACAGACTCCTTCTACT
 ATGAGAGCTTCCCTGACCGTGACCCATAAATCTGCTTTGGTGACGCGGATGGTACTGTGAACCTGAAGAGTGCCC
 TGCACTGCCAGGCTGGCAGAGCCGCCAGGAGCACCAAGTGTGCTGCAAGGAGCTGCCAGGACGAGGACATGG
 AGATGCTGGCCAAACGCCACCACTGGCTATCTGAAACGTGTGCTCTTGGGCGCTGACTCTCTGTGCCACAGGA
 CTCCTGTGGCTCGGCGGTGACCTGCTGTGGCTCTGGGGCTGCTCATGGCCACGCGTTTGGCAAAGTTTGTGA
 CTCACCAATCAAGGCCCGAGTCTGGACTGTGAAGCATCTGCCATGGGGAAGTGTGTTTGTATCTCTTTCTCT
 GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAGGGACACTGGATGGCAAGATGCTGCTGATGGTGA
 ACTGCTGTGAGCTAGGACTGGCTCCACAGGGTGGACTGGCTGGGGCTGGTCCAGTCCCTGGCTGGGGCATG
 TGTCCCTTATCTCTGTGGCTTTTCATCTGCTACTGGGCCCTGGCCCCGAGGCTTCTATGAGGGATGTT
 ACTGGGCTGGTCTGTGATCCAGAGGTCCAGGGATCGGCTCCTGGGCCCTCGGCTGACCTTCCACACACCA
 GCCACAGATAGGCGCTGCACCTGTGCTAGCTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC
 TGACTGGCTTCTGGGCGAGCCTAGCTCTCTCCCTTACACACAGGAGCATTAAGCTCTGGATTGGGCGAGCATGTG
 CCTGGGACATCTCACTCCACTCTCACTCCCTTACACACAGGAGCATTAAGCTCTGGATTGGGCGAGCATGTG
 CCCCCAGTCCCCGAGGCTGTGTTCCAGGGGCCCTGATTTCTGAGATGTGCTATGGCCCCAGGACTGAAGCTGC
 CTCCTTCACTCTGGGACTGTGGTTCCAGGATGAGAGCAGGGGTGGAGCCATGGCTTCTGGGAACCTATGGA
 GAAAGGGAATCCAAAGGAGCAGCCAGGGCTGCTCGAGCTTCCCTGAGCTGCACTCTTGCTAACCCACCATCA
 CACTGCCACCTCGCTTAGGCTCTCACTAGTACCAAGTGGGTGAGCAGAGGCTGAGGATGGGGCTCCTATCCAC
 CCTGGCCAGCACCCAGCTTAGTGTGGGACTAGCCAGAACTTGAATGGGACCTGAGAGAGCCAGGGGTCCCC
 TGAGGCCCGCTTAGGGCTTCTGTCTGCCCCAGGGTGTCCATGGATCTCCCTGTGCGAGCAGCATGGAGAGT
 CAGGGCTGCTCTCATGGCTAGGCTCTAAGTGGGTGACTGGCCAGAGCCGAGAAAGAGTACAGCTCTAGGT
 GGGGTTCCCAAAGAAGCCCTCAGGCTGAGCTGAGCTGCTCCCAACAGGGTTTCTGTGCGAGCTGAGATTTCTCTG
 TTGCATACATGCTGGCATCTGCTCCTCTGTTCTGAGTGGCCCCCATGGGCTCTGAGCAGGCTGTATCTCG
 GATTCTGGCAATAAAGTACTCTGAGTGCTGTAACAAAAA

09978375.101601

FIGURE 59

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189

><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

MGLHLRPYRVGLLPDGLLFLLLLLMLLADPALPAGRHPFVVLVPGDLGNQLEAKLDKPTVVH
YLCSSKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGDVVRVPGFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIIEMYQ
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI
PVIQPLKIREQQRSAVSTSWLLPYNTWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWLM
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCC
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

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FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGACGCGGCGGACGCGCAGATGGAGAGCGGG
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGACGCCGA
GGTGGTGGCGCGCGCGTGTGCTTGGTCTTCGCTTGATCGTGTTCTCCTGCATCTATGGTG
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTGGT
GGTCGACGCGTATTTCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGTTTGTGTTTCTGCTTCCTACCAAC
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGTGGGGGCGACTCTGTGAGGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT
GCCTACGCCCTCTTACCCAGGTGCATCTGTGGACAACACCAACAGCCACCCTTACCCAGAA
CGCGGAGACCACCGAGGGCTACCAGCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGA
GGGGGACAGAGAGGGCCCTCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCA
GCCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAAATGA
CCTCAGCCCCGCTGCGAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT
CAGCTTCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGCCATCACACCTGCCCTGTGCAGCGAGCCGACCAAGCTCTTGTGTCTCA
CTCAGGTTTGCTTCCCCGTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT
GGCTCTGGGCTGCCCTCCCGTGTGTGAGGGCGGGCTGGTGCTCATGGCACTTCCTCCTTG
CTCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCAGCTTTATGTAATATTC
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCATGGCTCCAGACTCTGTG
TGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGTGTTTGGAGACG
GAATAAATGTTTTCTCATTCAAAG

09733540604

FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24810, pI: 4.75, NX(S/T): 1
MESGAYGAAGAGGSFDLRRFLTPQVVARAVCLVPALIVFSCIYGEYGYSNAHESKQMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIIGDLLFSALWTFLWFGFC
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

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ACGACCACTACGCTGTCTCTAGAGCCAGGCGCTCAGGGGCTCATCGCCAGAGGGTGATCAGTGACAGGAAGTAT
CCGCTGGCTACGGGCCCCCAGACGTGGCTGTCGGCAGAGGGGACAGAGGTGATGCGAAGGAACCGAGCACAGAGGG
ATGTTTCAAGGCGCTGTGAGGACTCTCAGAGAACAGCCCGGGGTACCTTCGCTCAGGTCGCCCTTCTTGTGCTGTGCT
GCCCTTCGCTGTGCTGCTGCTGCTGCGCGGGGGTACTCTGGTATTTCTCTAGAGGTACAGCGAGAGTGATGTGTACG
CAGGTTGTACTCAGGACGATCTCGCTGTACTCAATCGCACTTCTCCAGGATCTTACCCTCGGGAGCTTACTGTGCC
TTCGCGACTGAAGAACCCGAAGGCTCAGAGAGTCTCATCAGCACGCCCTCGGGAACTTACTAC
AACTCAGCTCCGTTATTTCTTTGGGGGGGAGCCCTCACTCGTCTTCTTGTCTCATTTCTCAAAATCCCGAG
CACCGCCGGCTGTATGTACAGCCCGAGGTGGTGAGGACACTGCTGTGTGAGAGAGTCTGCTCCAGACTCAACAG
TCGGCTCCGCTTCCCTCAGGCGCCAGTACAGAGTGAGCCCGAGGGCTATGATGATCTGGAAGCAGTGTGAA
GACATAGCTGTCAATGAAATTCACGCTCGGTTGTATACGCTACAGATCAGTGGCCAGGGCCAGGTCCTTCGGGCT
AAGGGGCTTGACACCTGCGCTCTCAGCTGCTGTGGAACCTCGAGGGCCCTCAAGGACCTATGCTCAAACTCGG
CTGGAGTGGACAGCTGACGAGTGTGCGGGACCCAGTACCGCATGTATAGCTGTGCGGGCCCTGGAGAAGAGGGCT
ATACCTCGCTGTGTACGGTGTGACGCGCCAGGAGGCGGCTGTGTGAGGTTCTGCGCTGTGGGGGCCATATGSCGCT
GTCTGTGAAGAAGGGGCTGTACAGACTATACAGACCCCTTCGTGCTCTCGCTCGACCGCGTGGTCTCTCAGGCTCTG
GAGTGAAGTACGCTGTGACAGACAGGCTGACCTCGAGGCGTCTCTCAGCACCCGTATCTCCCGACACTAC
TGCCGCCAAACCACTGCTCTGTGGCACTCAGGTTGCCCTCTTGACATAGCTGTGGCCCTGTGTTGTATGTG
TATGACATCGAGGAGGACAGAGTATGATTGGCTGTGACCAAGGCGCAGTGAGACATCAGGAACAGAGGGTGTGT
GGCTTGGCATCTTCGACCGCTTACGCGCGAGAGGATCCCGTGTGGCCACCGCGGGATACCATCAACTCTCCCT
TCCGAGATCTCCCTTCAACGCGGCCGTTGCGGGTGACATGTGCTTGTATCAACCACTGAGGCCCTCGCCGGA
GAGTTCTCTCTGTGTGTATGGACTCTGTGTCTCGCTGTGTATGGGTTCAAGAGTCTGCCCAAGCGCTTGAAT
GAGAGAAATTCGCTTTGTACAGGCCAATTCCAGTGCAGAAAGAGACAGACATCTATCTCACTCCAGCCAGGTTGT
TTCGCGAGCTGATTGCTTCAACGAGACGATCAAGAGACAGTCTCAGGAAGGGGTGCTATGTGGGACATTCACC
ATTGAGTGTGAGGAACCGAGAGTGCCTCGAGAGGCCCAACCGCAGTGTGATGGGCGGCCGATCAGGGAAGGCG
TCGGATGAGGAGCACTGTGACTGTGGCTTCAGGCGGCTCCAGCCGATTTGTGTGAGCTGTGCTCTCCGAG
GGTGAAGTGCCATGGGAGCGGACGCTCAGGTTCCGGGTGCACATCTGTGGGGGGCCATCTACGTCATACCG
TGGGTGATACAAGCTGCGCACTGCTTCAGGAGGACAGCATGSCCTCCACGCTCTGTGACACCTCTCTGCGG
AAGGTTGTGACAGCAATCGCTGCTGGCTCGGAGAGGTTGCTTCAAGTGTGAGGCGCTGTCTGCATCCGTCAC
GAGAGAGACAGCAATGACTACAGCGTGGCGGCTGTGAGCTTCGACACACCCGTTGGTGCCTCGGCCGCTCGGCC
CCGCTCTGCTCTCGCCCGCGCTCCGCTCACTTCTCTCGAGCCCGGCTCTCACTGTGATATACGGGCTGGGGCCCTTG
CGAGGGGCGGCCCTCATCAGAACGCTCTGACAGAAGTGATGTGAGTTATCCAGCAAGCTGTGTGACGCGAG
GCTCTATCGCTACAGGAGTGACGCCACGATGCTGTGTGCGGCTACGCGAGGGCAGGAAGGATGCTCTCAGGTT
GACTCAGTGTGTCCGTTGTTGTGCAAGCACTCAGTGGCGTGTCTTCTGCGGGGCTGTGTCACTGGGCGCTG
GGCTTGTGGCCGCTCAACTACTTTCGGGCTCTACACCCGATCAGAGTGTGATCAGTGTGATCCAGCAAGTGTGT
ACTGAGAGTACCTGCCCTCTCGAAAGCAGGCGCCACTCTTGACTCAGAGAGCCAGGCACTCGGAGCACTCGAACAG
GGGACAGAGTATTTGCGCGGGGCTGGGGAGAGAGCGAGCCCTCTGTGTGCGAGAGTGTGCATCTTGTCTCTGCT
CTAGTGTCTGCTCAGTGTATGCGAGAGGATGAGAGAGTGCCAGCACTGGGGTGTCAAGACGCTCCCTCGAGGAC
CAGGCGCCACACCGAGCCTCTCTGCTCCCAATCTCTCTCTCGTCCCTCTTCTCACTGTCTGCTCATAGGCAAG
CGAGTGGTCTCAGAGCAAGAAATGCTGGTTCTATCACTCGAGAGATGTGTAGGTGGGCCCATCTGTGATCAGG
CTTTTGGGACGCTTGGCTCTCAGAGAGCAGATTCAGCTCTCGGAAGCCCTGTGTCTAACTTGGGATCTGGGAAT
GGAAGTGTCTCCATCGAGGGGAGCCCTCAGAGCCTGAGAGATGCGAGTGGGCTGTGCTGCACATGTAGAAGCAA
AAGTGGGAAGTCTCGACTCAGAGGCTCTGCCCAACCTCGTGGCTGACCACTGGGCTCTCAGAGCCAGACCCCT
CACTGGGAGTGTGACTCAGCTGCCCTTTGGAATAAAGCTGCTCTCAAAAAAATAAAAAAAAAAAAAA

FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGGQGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSQVYSGSLRLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT
YINSSSVYSFGEGPLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVLRLLKGPDLHLASSCLWHLQGPDKDML
KLRLWTLAECRDLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVFQACEVNLTLDNRDLSQGVLPSTPYFPSYSPQTHCSWHLTPVPSLDYGLAL
WFDAYALRRQKYDLPTCQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRA TFQCKEDSTCIS
LPKVC DGQPDCLNGSDEEQCQEGVPCGTF TTFQCEDRSCVKKPNPQCDGRPD CRDGSDEEHCD
CGLQGPSSRIRVGGAVSSEGEWPWQASLQVRGRHICGGAL IADRWVITA AHCFQEDSMASTVL
WTVFLGKVWQNSRWPGEVSKVSRLLLLHPYHEEDSHDYDVALLQLDHPVVRSA AAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDL CSEAYRYQVTPRMLCAGYRKG
KKDACQGDSSGGLPVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQVV T

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC
TAGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT
CTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTAACAACAGTCGGACCCCTGCC
CTGGAGAGTTCTCTGTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGACAGAGCCACATTCCAGTGCAAAGAGGA
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG
AGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGA
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGATTTGTTGGTGGAGCTGTGT
CCTCCGAGGGTGAGTGCCATGGCAGGCCAGCCTCCAGGTTCCGGGTGACACATCTGTGGG
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT
GGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG
GAGAGGTGTCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACACGAAGAGGACAGCCAT
GACTACGACGTGGCGCTGTCTGCAGCTCGACCACCGGTGGTGCCTCGGCGCGCTGCGCCC
CGTCTGCCTGCCCGCGCTGCCACTTCTTCAGAGCCCGCCTGCAGTGTGGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG
ATCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC
CGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGTGACTCAGGTGGTCCGCTGGTGTGCA
AGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCACTGGGGCTGGGCTGTGGCCGG
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCCCACCTCCTGGACTCAGAGAGCCAGGGC
AACTGCCAAGCAGGGGGACAAGTAT

0976275.101604

FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACGCCCCGGG
CTCCGTGCCGCCAAGTTTTCATTTCACACCTTCTCTGCCTCCAGTCCCCAGCCCCCTGGCCG
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGGTGGTTTTTGTTTTTTAAA
ACTTCTGTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCGTTCCTCTGCTCTG
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG
TTTAACTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGTACCTCTCCGTGGCCACAG
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAAACCTTTTTTCATCATTACGGAT
GGACGATGAGCGGTATCTTTGAAAACTGGCTGCACAACTCGTGTGAGCCCTGCACACAAGA
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCACCAGCTTTACACGGA
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG
AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC
CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG
TGGATGTCTCCACACCTACACGCGTTCTTCGGCTTGAGCATTTGGTATTAGATGCGTGTG
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCAGCCAGGCTGTGGACTCAACGATGT
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAATGTGAGCATGAGCGAGCCG
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTGCCITTCAGTGCACT
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT
TGGCTACAATGCCAAGAAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG
CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA
CCTCCTTCTTAATACCATGTGTCAGAGCAGGGCAGCATCCTAGCCAGGAGAAGTGGCCAGCA
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCTAGGAAAGGGAATCTTT
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTVEVKPSVRFNLRRTSKDPEHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVVDWL
PLAHQLYTDVANNTRVVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV
GRITGLDPAGPMFEGADIIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDLSVNQDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

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090587-1

[illegible]

ORDERED

<MW: 76193, pI: 5.42, NX(S/T): 4

amino acids 411-431, 152-171, 331-350 and 374-393

FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGATAACGTGCAGCCGAAAATAAACATCGCCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGTTATTTTGGCCTTTGCTTGATAT
TATCAACTCACTGGTAACAACAGTATTTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCAGCGGTCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAGAAGTTTGTAAATTTTATATTACTTTTATAGTTTGATACTAAGT
ATTAAACATATTTCTGTATTCTTCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645
><subunit 1 of 1, 152 aa, 1 stop
><MW: 17170, pI: 9.62, NX(S/T): 1
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTEFFIIAQAPEPYIVITGFEVTVILFFILL
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTLTVGGGVFALVAVCCCLAD
GALIYRKLLFNPSGPFYQKKPVHEKKEVL

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

00978375.101601

FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAAC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC
TGAACCATATATTGTTATCACTGGATTGAAGTCACCGTTATCTTATTTTTTCATACTTTTAT
ATGTACTCAGACTTGATCGATTAATGAAGTGTTATTTTGGCCTTTGCTTGATATTATCAAC
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTTGACAGCAGTATGCTGTNTTGCCGAC

0978375.101601

FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGCCCCCGCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC
CTCTGCTGGCCAGTGGCTCCTGCGCGCGCCCCGGAGCTGGCCCCCGCGCCCTTACGCTG
CCCCCTCGGGTGGCCGCGGCCACGAACCGCTAGTTGCGCCACCCCGGACCCGGGACCCCC
TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCCTGCCCTGGCGTCCCCCGCG
GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT
CTAGCACATACCGCTCCAAGGGCTTTGACGTCAAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGGAAGACCTCGTACCATCCCCAAGGCTTCAATACTTCTTTTCTGTCAA
CATTGCCACTATTTTGAATCAGAGAATTCTTTTGGCTGGGATTAATGGAAATGGAATAC
TTGGCCTAGCTTATGCCACACATTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC
CTGGTGACACAAGCAAAACATCCCCAACGTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCG
AAATTGGAATTTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG
AAGCTGTGGCCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG
CTGGCGTGTCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAAATCTCCATCTACCT
GAGAGACGAGAATCTCAGCAGGTCAATTCGTATCACAATCCTGCCTCAGCTTTACATTACG
CCATGATGGGGCCGGCCTGAATTATGAATGTTACCGATTGCGCATTTCCCATCCACAAT
GCGCTGGTGATCGGTGCCACGCTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCAGAA
GAGGGTGGGCTTCGCAGCGAGCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCTTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT
AATCGTCTGCTGCTGCTCGGTTCCGGTGTGAGCGTCGCGTCGCCCCGTGACCTGAGGTGCTCA
ATGATGAGTCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA
CCATGAACCTCAGCTATTAAAGAAAATCACATTTCCAGGGCAGCAGCCGGATCGATGTTGGCG
CTTTCCTGTGCCACCCGCTCTTCAATCTCTGTTCTGCTCCAGATGCTTCTAGATTAC
TGTCTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA
AAAAAAACTTCATTCTAA

FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLPLLAQNLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGLAL
ALEPALASPAGAAFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFVAVAGTPHS
YIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNSTSLVNIATIFESENF
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS
LVLGGIEPSLYKGDIIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLR
LPQKVFDVAVVEAVARASLIPEFSDGFWTGSQSLACWTNSETPWSYFPKISIYLRDENSSRSFR
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA
EIAAAVSEISGPFSTEDVASNCVPAQSLSEPIILWIVSYALMSVCGAILLVLLVLLLPFRCL
QRRPRDPEVVNDESSLVRHRWK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

FIGURE 74

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCGGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCCTGGCGCGATCCAGGGCGGTGCGGGCCTGGGCGGGAGCCGGGAGGCGCGGCC
GGCATGGAGGCGCTGCTGCTGGGCGCGGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA
CAACCTGGTGAAGGCCCCGCGCTGCGGCGGCATGGGCAACCTGCGGGGCGCACGGCCGTGG
TCACGGGCGCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG
CGCGTGTGCTGGCTGCGCGAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTTCATCTTCATGGCCTTGGAAGTGGCCAGTCTGGCCTCGGTGC
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC
GGTATCAGTTCTGTGGCCGGACCCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT
CGGTCCCTTTCTGTGACACATCTGTGCTGCCTTGCCTGAAGGCATGTGCCCTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCACTGTGCGGGACGTCTTGACTTCAAAGCCTGGACCGC
CAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGGCCCGGAGCTCGCCCAACGAGCTTGAGGCCACTGGCGTCACTGCTATGAGCCCAAC
CAGGGCCTGTGAACCTCGGAGCTGTTCTGCGCCATGTTCTGGATGGCTGCGCCCACTTTTG
CGCCCATGGCTTGGCTGGTGTCTCCGGGCACCAAGAGGGGGTGCCAGACACCCCTGTATTG
TGCTCTACAAGAGGCATCGAGCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG
AGGTGCCCTCCAGCTGCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCTGGGGAGGATGCTGAACCGATGAAGACCCCAAGTCTGAGGACTC
AGAGGCCCATCTTCTCTAAGCACCCCCACCCCTGAGGAGCCACAGTTCCTCAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTGTCTAAGATGACGACCCGAATTGAGCTAAAGTTGAG
CCTGAGATCCAGCTCTCCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTGGATGTAGTATTTTCAGGCCCCACCTTATTGATCTTG
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG
TGAAGTATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG
GAATTAGGCTCCCGAGCTAAGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG
GGATCTGAACCCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAAGATGGGTGCTGAGAAGTGA
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG
ATGCAGGGCTGGGTTCATCTGTATCTGAAGCCCCCGGAATAAAGCGCGTTGACCGCCAAAA
AAAAAAAAAAAAAAAAA

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FIGURE 75

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYVNLVKAPPCGGMGNLRGRTAVVTGANSIGIGKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNA
ISSCGRTREAFNLLLRVNHIGPFLTHLLLPCLKACAPSRVVVVASAAHCRGLDFKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPNSEFLRHVPGWLRPLLR
PLAWLVLRAPRGGAGTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHLWEASKRL
AGLGPGEDAEFDDEDPQSEDSEAPSSSLSTPHPEEPTVSPQYPSPPQSSPDLSKMTHRIQAKVEP
EIQLS

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

097875.10101

FIGURE 76

GGAGGAGACAGCCTCTCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCTGCTCATCATGGGGAGGCATGGCTCAG
 GACTCCCOCGCCAGATCTCTAGTCCACCCCGAGGACAGCTGTTCCAGGGCCCTGGCCCTCCAGGATGAGCTGC
 CAAGCCTCTCAGGCAGCCACTCTCCACCATTCGCTGGTTGCTGAATGGGCAGCCCTGAGCATGTGTCGCCAGAC
 CCACACCACTCTCTGCCTGATGGGACCTTCTGTGCTCAGAGCCCCCTGCCCGGGGACATGCCACGATGGCCAG
 GCCTGTCTCAGAGACTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGACCGGCAGTGCAGAGAGCGCT
 CGGCTGTCTGTGGCTGTCTCTCCGGGAGGATTTCCAGATCCAGCTCCGGACATGGTGGCTGTGGTGGGTGAGCAG
 TTATCTCTGGAAATGTGGGCCGCTCTGGGCCACCCAGAGCCCAAGTCTCATGGTGGAAAGATGGGAAACCCCTCG
 GCCCTTCAGGCCGGAAGGCACACAGTGTCCGGGGGGTTCCTGCTGATGGCAGAGAGAGAGAAGTGAAGGAGG
 ACCCTACATGTGTGGGCCAACCAACGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGGTTTCCATTCAGGAGCCC
 CAGGACTACACGAGGACCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAATGTGACACTGTCTGAACCCGGAT
 CCTGCAGAGGGCCCCAAGCTCAGACCGGCGGTGTGGCTCAGCTGGAAAGTCAGTGGCCCTGTGCGCTGCCCCAA
 TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGCTGTCTGGCC
 GGCTGGCAGAGCGCAGAGCTTGGAGGCTCCTCACTGGGGCCAGAGCTACGAGTTCAAAGTGAGACCATCTCTGGC
 CGGGCTCGAGGCCCTGACAGCAACCTGTGCTCTCTGAGGCTGCCGGAAAAAGTGCACAGTGGCCCCACCTCAGGAA
 GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCACCACCTGTCTGAAAAACCAATGGCATC
 ATCCGTGGCTACAGGCTCTGGAGCCTGGGCAACACATCTGACCACAGCCAACTGGACTGTAGTTGTGTGAGCAG
 ACCCAGCTGGAAATCGCCACCCATGTGCCAGGCTCCTACTGCGTGAAGTGGCTGCAGTCACTGGTGTGGGCTG
 GGGGAGCCCGATAGACTGTCTGCTCTCTTTAGAGCAGGCCATGGAGGAGGCCACCAAGAACCCAGTGAAGAT
 GGTCCCTGAGCCCTGGAGCAGCTGAGGCTTACCTTTGAAGCGGCTGAGGTTCAGCACTCGCGGTGTGCACTC
 TGGCTGTGCTCTGGGACCGCCCTGTGTATCCACCGCGGCGCCGAGCTAGGGTGCACCTGGGCGCAGGTCTG
 TACAGATATACAGTGGAGGTACCTCCATAAAACACAGGATGGATCAGACTGACTCCAGTGGTGTGGCAGACACT
 TGGCCTTCCACTCTGGCTCTTCGGACCTGAGCAGCAGCAGCAGCTCAGCAGCTCGCTGGGGGGGATGCCCGG
 GACCACTAGACTGTCTCGCTCTCTGTCTCTCTGGGACTCCCGAAGCCCGGCGTGCCTGTCTTCAGACACC
 AGCACTTTTATGGCTCCCTCATCTGCTGAGCTGCCCTCCAGTACCCAGCAGGCCAAGTCCCAGGTGCCAGCT
 TCAGGCGGCTCCACCCAGCTGGCCAGCTCTCCAGCCCTGTCTCCAGCTCAGACAGCTCCTGCAGCGCCAGG
 GGACTCTCTCTCCCGCTGTCTCTGCGCCCTCGACAGGCTTGGAAAGCCAAAGACAGGAGTTCGACGAT
 GCGCAACGTTCGCCACTGCTCCGGGCGAGCCTCTTGGAGCTCCGGGCTGTGAGGTGAGCCATGAGGTTC
 AAGAACCTTTCCCAAGGCCAGGAGCTGTGCCCTCAGCCTCCTCTTCTCAGTAACTCCCACTCAGCT
 AGCTCCTCAAATGAGCTGGTTACTCTGTCTATCTCCCTCCAGCAGCCCTCTTCTCCTCAGTAACTCCCACTC
 AGTCAACAGACCCAGCTCCCGGTGGCACCAAGGCTCCCTCCTCCTCTGCTGCCAGCAGCCCACTCCCACTC
 CTTAGCCCTTCAGCTCCCTTAGCCCCAGGCTCTTCTCTCTGCGCCAGGCCAGCTCCAGTCCGCTGTTC
 AGCTCCTCAGTGTCTATCCCTGGGGAGGATCAAGACAGGCTGTGACCTCCAGGAGGTAGCCCTGTGCTTGGAA
 CTCAGTGGAGGTGAGGAGACTCCAGGAACAGGCTCTCTCCATGCCAAGGGCTCTTCAACCCCAACCACTAT
 GGGTACATCAGCGTCCCAACAGCTCAGAGTTACGGAGCATGGGAGGACTGGAGGAGGGGTGGGGCCCAAGGG
 GAGTCTGTGCTGTGCCACTCTCGGCCCTGCCTACCCCAACCCCGAGCAGGGCTCTTAGCCAAATGGTGTGGGC
 TCAGCTCTGAGGACAAATGCCCGCAGCGCCAGAGGCCAGCTTGTGAGCTCCTTCAGTGGCTCTCTCTCGCTGAT
 GCTCACTTTGCCCGGCCCTGGCAGTGGCTGTGGATAGCTTTGGTTTCGGTCTAGAGCCAGGGAGGAGCAGACTGC
 GTCTTCATAGATGCTCATCCTCAGCTCCCTCCCAAGGATGAGATCTTCCAGCCCAAGCTCTCTCTCGCCCTG
 TGGAGTGGAGGCCAGACTGGTGTGAAGACATGGAGGTGAGCCACACCCAGCGCTGGGAAGGGGATGCTCTCC
 TGGCCCCCTGACTCTCAGATCTCTTCCAGAGAAGTCACTGTGCTGATGCCCAAGGCTGGTGTCTCTCT
 GTAGATTACTCTGAACCGTGTCTCTGAGACTTCCAGAGCGGAATCAGAACCACTCTCTGTCCACCCACAG
 ACTGGGCTGTGCTGTGGGTCTTGGGCTCTTGGCCCTGTGTTCTCTGAGCTGGGGTCACTTCCCAAGCTCCAGAG
 TTTCTCCCTCAGCAATGTGAAAAACAAATGAAAAACAAATTAGAGCAAGCTGACCTGGAGCCCTCAGGAGCAAA
 ACATACCTCAGCTGACTCCTACCTGACTGCTTTCTCTCTGTGCCATCCACTCCCAACCAAGTGTCTTTTGGC
 CTGAGGAGCAGCCCTGCTGTGCTCTTCCCCCACTATTGGATCAGAGGAAGTGGAGGAGCCAGAGGTGCTT
 GTGGAGGACAGAGTGGCTGTGGGAGAGGGCTGTGGAGGAAGGAGCTTCGGAGCCCTCTCAGGCTTAACCT
 GGGCCCTCTCTAGAGAAAGACTCAACTCTCTCCAACTCACCATGGAAGAAATAATATGATGACCACT
 AGGCATCAGGCCCTACTCTATGCCAAACAAAGGTTCAAGCTGGGTCTAGGAGTCTGAAGGAAGGGAGG
 TATGAGACCGTAGGTCAAAGCACCATCTCTGTAAGTGTGTCACATTAAGCTTAAGAAATTTGATACCAATAAAT
 GGTAAAAA

09978375.101501

FIGURE 77

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGMAQDSPPQILVHPQDQLFQGGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLP
DGTLLLLQPPARGHAHDGQALSTD LGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMCV
ATNSAGHRESRAARVS IQEPQDYTEFVELLAVRIQLENVTL LNPDPAEGPKPRPAVWLSWKV
SGPAAPQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLRLPEKVPSPAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP
ANWTVVGEQTQLEIATHMPPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGFW
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWSRSRSPGVPLLPDTST
FYGSLIAELPSSTPARPSPQVPAVRRLPFPQLAQLSSPCSSSDSLCSRGLSSPRLSLAPAEA
WKAKKKQELQHANSPLLGRSHSLELRACELGNRGSKNLSQSPGAVPQALVANRALGPKLLS
SSNELVTRHLPPAPLPFHETPPTQSQQTQPPVAPQAPSSILLPAAPILSPCSPSPQASS
LSGSPASSRLSSSSSLSGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRITGGGVGPKGGVLLCPPRPCLTPTPSEGLANGWGSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLPREADCVFIDASSPPSPRDEIFLTPLNLSLP
LWEWRPDWLEDMEVSHQTQRLGRGMPPWPFPDSQISSQRSQLHCRMPKAGASFPVDYS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

0078375-101604

FIGURE 78

CTCCCCAGGTTGCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAGGGGCACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGAGGAAGGGT
 GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAGAAGAAGGCCAGAGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCCTGTGGA
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCGCATGAG
 TCTTTACTGATCTCTGTGTCGTTTCCAGGACCTGCTGTCTCCCTCCCTTCTCCAC
 CTTCCAGCCTCTGGCTACAACAGCCCTGCAGCCCAAGGCAAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCAAGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCTCACCCAGCGACCTCTCTCTGCAAGGAGCTCCCGCCCCCATGCAAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTCTGGTGTGCTGAGCCTTCTGTGAGC
 CGCAGGCCCTGATCGCCTTCTGCAGCCACTGCTCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCCTTGACTCGGAGGAAAAAGGAAGCC
 CTTTCCAGGCCCTGAGGGGACGTGATCTCGATGCTCTCCCTCCCTCAGCAATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTCCACCTCAGCTCCAGAG
 TCCAGCTGCCCGAATCCAGGGCTCTCCCAACCCTCCCAAGCTCTCTCTTGTGATGTTTCCA
 GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCAGAGCGGTGGCCTTGTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCPCA
 GCAGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACTCTGGGG
 CTCATGCCCAGTGTGCGACCTGCTCTCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCCACGGTCTCTGCACTCAGCTGGTGTGTAAGAGGAGCAGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTTCAGGAAGCCT
 GTGAAAAACGTGATTCTTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGAG
 GACTCTGAATTTAAACAATGCCAGTGACTGTGCGCACTTGAGTTTGAAGGCCAGTGGGCCGTG
 ATGAACGCTCACACCCCTTTCAGCTTAGAGTCTGCAATTTGGGCTGTGACGTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCCTGCTAAG
 TCCAGGCCCTTGGTCAGGTGAGGTGCACATTGCAGGATAAGCCAGGAACCGGCAAGAAGTGG
 TTGCCCTTNNCCATTTGCCCTCCCTGGNCCATGCCCTTCTTGCCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCTTCTTCTTCTGCTGGAAGGGTTACTTGCCTATGGGTTCTGGTGCTAGAGA
 GAAAAGTAGAAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGGGGGTGGTGGTAAAGTA
 GCACAACCTACTATTTTTTTCTTTTCCATTATTTGTTTTTAAAGACAGAATCTCGTGCT
 GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCCTCTGGGTTCAAGTGATT
 CTTCTGCCTCAGCCTCCGAGTAGCTGGGATTACAGGCACGCCACACCACTGGCTTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGCCTCTCTCTCAGTCTCCCAAATTTGCCGGGATTACAGGCATGAGCCAATGTG
 TCTGGCCCTATTTTCTTTAAAAAGTGAATTAAGAGTTGTTCAAGTATGCAAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT
 TATTTCTGTTTGTGTAATCTCTTCCATCTTTTCTTCTCACATAATTTGCCGGTGTCTT
 TTTACAGACATAATATCTTGATATACAACCTTTGATCTCTGCTTTCACCTTATCGTTC
 ATCACTTTATTCAGCACTTCTCTGTGTTTACAGACCTTTTATAAATAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

09978375-101601

FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIIRDSRQELSLIVTLWNLTLDAGEYWCVEKRGPDSESLISLFV
FPGPCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPAGSSRPQMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPPLHTSEELGFSGFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

00978375-10104

FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTATCCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGGCGGTGGTGCCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTTTCAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGAGCAACCTCACCCGAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTCTAGGATGGACGGAACCATGCA
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA
AAGGATGGTTGAACGTGAAA

0978375.201604

FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNGIFQINSRRWCSNLTPNVPNVCRMVCSDLLNPNLKDTVICAMKITQEPQGLGY
WEAWRHHCQGGKDLTEWVDGCD

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

0978375-101601

FIGURE 82

AGCCGCTGCCCCGGGCGGGCGCCCGCGGCGGCACCATGAGTCCCCGCTCGTGCTGCGTTCC
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA
AGCTGTGTCGTCGGTGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCGGGAACCGGCGCTGGAAGTGTCCACAC
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACCGGGCGTGCGAGAGTGGGGAGCT
GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGGTCAGCCCAAGGGCTTCAGTGGTCAAG
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCAGTCTGTTTGTGGATGTGCGGGAG
AGAAGCAAGGGGGCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCGCGCAG
GAAGGCCATCCTGACACACATGCGGGTGAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCGGCCAGGTGGGTGACGCACTGAAGGAG
AAGTTTGATGGTGGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCTCCAGGGCACTGGTACC
ACGCAACGCACAGTTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG
ACTTCTGTGAGCAGGACATGCGCAGCGCGTGTGGGCACGAGGGGCGGCACATGCAACAAG
ACGTCCAAGGCCATCGACGGCTGTGAGCTGTGTGTGTGGCGCGGCTTCCACACGGCGCA
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCAGTGGTGTGTCTTCGTCAAGTGCCGGC
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGAGCCGCTGCCTAGCCCTGCGCCGGC
AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCACCACCTACCCCAAGA
GATACTGGTTGTAATTTTGTGTTCTGGTTTGGTTTTGGGTCTCATGTTATTTATGCGCGAA
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAGCCTGGGCCTTTGTGGCT
GCCACTGACCAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGTGGAGTAACAAGGAGTAT
TACCACCACATGGCTACTGACCGTGTCTATCGGGGAAGAGGGGCGCTTATGGCAGGGAAAAA
GGTACCGACTTGATGGAAGTCACACCTCTGAAAAAAGAACTTTAACTCTCCAGCACACA
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAG
GAACAAGCAGATAACCAAGTCAAGGGCACCAAGGTTCAATTCAGCCCTTACATGGACAGCTAGA
GGTTCGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA
GTCCCAACCTAGAACCCAGCCTGCCCCAGCCTGCCCTGGGAAGAGGAACTTAACCACTCC
CCAGACCCACCTAGGCAGGCATATAGGTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT
TGCAGTCATGCCGAGTCACCTTTCACAGCGCTGTCTCCATGAAACTGAAAAACACACAC
ACCTGCGAGA
GAGAGGGAGGAAGGGCTGTGCCTTTCAGTCTATGCCGAGTCACCTTTCACAGCACTGTTCCT

00073375-101601
100101528260

00000000

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328
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<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLSRLRLLVFAVFSAAASNWLYLAKLSSVGSISEETCEKLKGLIQRQVQMCKRNLE
VMDSVRRGAQLAIECQYQFNRNRNWCSTLDSLVPVGKVVTTGTRERAAFYVAISSAGVAFV
TRACSSGGELEKCGCDRTVHGVSPPQGFQWSGCSDNIAYGVAFSQSFDVRRERSKGASSSRALM
NLHNNEAGRKA I LTHMRVECKHGVSGSCEVCTCWRAVPPFRQVGHALKFKFDGATEVEPRR
VGSGRALVPRNAQFKPTDEDLVLPSEDFCEQDMRSGVLTRGRGTCNKTKSAIDGCELLC
CGRGFHTAQVELAERCSCKFWHCCFPVKRCQCRDLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATGGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGTCCC CGAGGGC
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGT CCTGGTC
ACCACAGTCTTTGGGCTGTGATTCTGAGTATCTATTGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGTGG
GTGCCCTGAAGGAGGAGGTCCGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAAGTGCCTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAATCCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCTTCGAGGGCTCCTGTACTTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGGATGAGCAGGGCTTCTCACTCGGAACACGCGTGCCGCTGTTACTGGCTGGGCCCTGAGG
GCTGTGCGCCATCTGGGCAAGGTTCAAGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAAC CAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGT CATGATGC
TG CACACGGGGCTGTGGAACGACGACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAATGCTGGACCCCGCCAGTGCCCTGGAGCCGCGCCATTGCAGCATGTGTA
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTTCCT
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCTAACTCCACTCACGCAGACCCAACTAACC
TCCACTAGCTCCAAATCCCTGCTCCTGCGTCCCGTGATATGCCTCCACTTCTCTCCCTAA
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTITCCACCAAACCTGGA
AGCTGTTTTTGAGCCTGAGGAAGCATCAATAAATATTGAGAAATGAAAAA

FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352
<subunit 1 of 1, 293 aa, 1 stop
<MW: 32562, pI: 6.53, NX(S/T): 2
MDTTRYSKWGSSEEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLKASTERAA
LLDGHDLRLTNASKQTAAALGALKEEVGDCHSCCSGTQAQLQTTRAEELGEAQAKLMEQESALR
ELRERVITQGLAEAGRGREDVRTLEFRALEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS
HWNQGEFNDAWGRENCVMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

0976375-103604

FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCTGCTGGGCAGGGCGAGTTGGGAAAGCG
GCAGCCCCCGCCGCCCCCGCAGCCCCCTTCTCCTCCTTTCTCCACGTCCTATCTGCCTCTCG
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACCTGGAGCCTCATTTGGCCGGCCCCGG
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCCTGCCGGC
CGCGCTCCCGCTGCTCCTGCGGGGTGATGGAAAAACCCAGCCCGGCCCGCCCTGGGCAAG
GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC
CATCTGTTCGCCAGAGCCCCGGCCAAATACAGCATCACCTTACCGGCAAGTGAGCCAGA
CGGCTTCCCCAAGCAGTACCCCTGTTTCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTCAGTAACGGGCTGCC
CGACTTTGCGGAGCGCGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGCGGGGGAGG
CGCTGCAGAGCGTGCACGAGGTGTTTTGCGCGCCCGCGCTCCCAGCGGCACCGGCGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC
TAGCCCCGACTGGTTCTGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTACCTTCTCC
TCCCCAACTTCCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCTCTCTCCAG
CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCAGTCTGCCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCAGAAACGCCGCTGGACTGCGAGGTCTC
CCTGTGGTCTGCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
CTCGCTACGTCGGGTCCAGCCCCGCAACAACGGGAGCCCCCTGCCCGAGCTCGAAGAAGAG
GCTGAGTGCGTCCCTGATAACTGCGTCTAAGACCAAGAGCCCCGAGCCCCCTGGGGCCCCCG
GAGCCATGGGTGTGCGGGGCTCCTGTGCAGGCTCATGTGTCAGGCGGCCGAGGGCACAGGG
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT
CTGTGGCCGCGACGGGCATTGGGAAACAGCCTCCTCCTTTCCAACTTGCTTCTTAGGGG
CCCCCGTGTCCGCTCTGCTCTCAGCCTCCTCCTCTGCAAGGATAAGTCATCCCCAAGGCTC
CAGTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCCTTATCG
TCCAGGGGCTGGCTCCACGTGGTTGCAGATACCTCAGACCTGGTGTCTTAGGCTGTGCTG
AGCCCACTCTCCGAGGGCGCATCCAAGCGGGGCCACTTGAGAAGTGAATAAATGGGGCGG
TTTCGGAAGCGTCAGTGTTCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

0978375.101601

FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAAHSSDYSMWRKNQYVVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFVGVDSLDCDGRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFIPPAPVLPSPRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKSRTRYVRVQPA
NNGSPCPELEEEAECPDNCV

Important features:

Signal peptide:

amino acids 1-26

0978375-101601

FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGCTCTTGCGTGA
TATTGACAAACTGAAGCTTTCTGCACCACTGGACTTAAGGAAGAGTGTA CTGTAAGCGGA
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAATGGGAAGGTTTTATTGAAAACTA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT
ATCCAACCTTTGTTGGAAAGCTTATTATGACAATACCATTTTTCATAGAGTTGTGCCTGGTTT
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTCAATCAAGGTTGCGTTTTTAATCGGAGAGGACTGGTGGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACTGGGTGCGAGCAGATGAAT
TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAATAAAAAGCTGT
GAGGTTTTGTTTTAATCCTTTTGATGACATCATTCGAAGGAAATTAAGGCTGAAAAAGA
GAAACCAGAGGAGGAAGTAAGAAATTGAAACCAGGACAAAAATTTTAGTTTACTTT
CATTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT
TGTAAGAAAGTAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTGTGATAAGAAACCTGATGAGAGAAAGAAATGCCAAAAAA
TAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAACCGGAACTCTTAGCAG
CAAAACAAAAAAGTAGAAAAATGCAGCAAAACAAGCAGAAAAAAGAAAGTGAAGAGGAAGAA
GCCCTCCAGATGGTGTCTTTGCCGAATACAGAAGAGAAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAAGGGAACCTCCCGGGAAGATCAGACCCTTGCACTGCTGAACAGT
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAATGACATTCTGAAACAGAA
GTAGAAGATGATGAAGGATGGATGTACATGTACTTCACTTTGAGGATAAAAGCAGAAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA
ATAAAGAAGGAGGGAAGAAAGCAAAAGCTGATGAGAGAGAAAAAGAAAGATAAAT
GAGAATAATGATAACCAGAACTTGCTGGAATGTGCCTACAATGGCCTTGTAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTGAACCTGTTGTCTGTTTTG
AAAAACAATTATCTTGTTTTGCATAATGTGGAATGATGTAAGCAATGCTTTTGGTTTACTGG
TACATGTGTTTTTCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCT
TCCACAAAAA

0970375-104601

FIGURE 89

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLTKTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEK
PEEEVKKLKPKGTKNFSLLSFGEEAESEEEVNRVSQSMKGKSKSSHDLKDDPHLSSVPV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKCLKDTSANVKSAGEGEVEKKS
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAAPPDGAVA EYRREKQKYEALRK
QQSKKGTSRDQTLALLNQFKSKLTQAIATPENDIPETEVEDDEGWMSHVLQFEDKSRKVK
DASMQSDTFEYIDPRNPVNKRREESKKLMREKKERR

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

0978375.101604

FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCGGTGCCGGGCGAGAGAGATGCTGCCCCG
CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCCAGACCCATTTCGGCTTGCTGACGGCGTGG
AGCCCTTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCCAG
GTGGCCGCCGGCGGGGACCAGCACAGGCGCGGTTTCTCCTTCGGAACGGGAACGTCTAGCAA
CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGAAGTACTTCACTCCAGCAACTACATCTG
CTCCTTCAAGTGGTTTTGGAAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGGTCTCACTCTA
GGAGGAACAAATACAGGTGCCCTTGCACACCAAGAGGCCCTCAAGTGGTCAACAAATATGGAAC
CCTGCAAGGAAAAAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTAGGAGTCCCTT
TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAA
GGAATCAGAGATGTACCACTTACCGCCTGGATGGAGTCTCGCTCTGTGCGCAGGCTGGAG
TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCTCCCGGGTCAAGCGAGTCTCCTGC
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCCTGCAGGAGTCTTGGGGCCAGCTGGCCTCG
ATGTACGTGACGACGCGGGAAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT
GAACGTGTACGCGCGCGCGCGCGCCGGGATCCCAAGTCCAGTGCAGTATGGTCTGGTTCC
CGGGAGGCGCCTTCATCGTGGCGCTGCTCTTCTGTACGAGGGCTCTGACTTGGCCGCGCCG
GAGAAAGTGGTGCTGGTGTCTCTGCAGCACAGGCTCGGCATCTTCGGCTTCTGTAGCACGGA
CGACAGCCACGCGCGCGGAACTGGGGCTGCTGGACAGATGGCGGCTCTGCGCTGGGTGC
AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTTCGCCAGTCCGGC
GGGGCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGC
CAATTTCCAGAGTGGCACCGGTTAATTGAGACTTTTCATCACTAGTAAACCATGAAAGTGG
CCAAGAAGGTTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTCCAAC
GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG
TGATCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT
CTAGGTGTCAACAACCTGGAATTCATTGGCTCTTGCCCTTATAATATACCAAGGAGCAGGT
ACCACTTGTGGTGGAGGATACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA
ACCGTATGATGGACATAGTTCAGATGCCACTTTGCTGTATGCCCACTGCAGACTGCTCAC
TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGTGGCCACGCTACAACAGGATGAA
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCACTGAAGCTCAAGGAGAAGAAGATGCG
TTTTTGGATGAGTCTGTACCAAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC
TGTGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA
TAGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTGAACATGCAGGAGCTCCCTGCT
GCCTCCAGGCCAAAGCTAGAGCTTTTGCCCTGTTGTGTGGACCTGCAGTGCCTTTCCAGCC
TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC
ACCACATGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTCCCTTCTCAAAATCCT
CCACCCCTTCAATGTCTCCTTGTGACTCCTTCTTATGGAGGTCAGCCAGACTGCCACTG
CCCTGTCACTGCACCAGCTTGGCATTTACCATCCATCCTGCTCAACCTTGTCTCTGTCTGT
TCACATTTGGCCTGGAGCCTAGGCAGGTTGTGACATGGAGCAAACTTTTGGTAGTTTGGGA
TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCAAAGTCTATACACAGGGGTGG
TCTCTTCAATAAAGAAGTGTGATTAGAAAAA

FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTIGSTTTVAAGGTSTGGVFSFGTGTSSNPVGLNFGNLGSTSTPATTSAPSSG
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTILQGKQMHVGKTPIQVFLGVFPFSRPP
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGQLASMYVSTRERYKNLRFSEDCLYLNVPYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLDQMAALRWVQENIA
AFGGDPGNVTFLFGQSAGAMISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLACNHNSTQILVNCLRALSGTKVMRVSNNMRFLQLNFPQRPDEEIIWSMSPVVDGVVIPDD
PLVLLTQKGKSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

0978375-101601

FIGURE 92

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT
GCTGTCTCTCGTCTGCTGGGCGGGTCCCAGGCATGATGGAGAGATTCTGGATACAGAGTCGAG
AGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCGA
CAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC
CAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGAGAGGTGGAATGAGCACC CGGGGCC
GATTCCAGCTCACTGGGGATCCCGCCAGGGGAACTGCTCCTTGGTGATCAGAGACGCGCAG
ATGCAGGATGAGTCAGACTTCTTTTCGGGTGGAGAGAGGAAGCTATGACATATAATTT
CATGAACGATGGGTTCTTTCTAAAGTAACAGTGCTCAGCTTCAACGCCAGCCAGGACCA
ACAAACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
GTCCGACTCCGTGTGGCCTATGCCCCAGAGACCTTGTATCAGCATTTACAGTGACAAACAC
GCCAGCCCTGGAGCCCCAGCCCCAGGGAATGTCCATACTTGGAAAGCCAAAAGGCCAGT
TCCTGCGGCTCCTCTGTGTGCTGTACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGCGAG
AACAGAGTCTCTCCTCGTCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCCG
GGTGAAGCTGGGGATTTCAGGGCCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGC
AGCGAGCCCTGGACCTCTCTGTGTCAGTATCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA
GCAAACAGGACAGTCTTGAAACCTTGGGAACCGCACGCTCTCTCCAGTATGGAGGGCCA
AAGCCTGTGCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA
GGGACAGGTTCTGAGCCCCCTCCAGCCCTCAGACCCCGGGGTCTGGAGCTGCCTCGGGT
CAAGTGGAGCAGAAAGGAGAGTTCACTGTCCACGCTCCGGCACCCACTGGGCTCCAGCACGT
CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGGATTCTCCAACGGAG
CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCTCTGCTGGCCCTGATCATATGAAG
ATTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCCCAGGTTCTCCCAGCACAGCAC
GATCTTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA
AAGCCACACCAAACAGTCTCGGACCCCTCCTCCACAGGTGCTCCCTCCAGGAATCAAAG
AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCTCAAGC
CCCAGAATCCAGGAGAGCCAAAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCA
GACCCAGGCTGAGGCCGGATGCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTT
CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTTCGGCTAGGAGGAGAGGTAGAGTAAGAG
GTTGAAGATAACAGAGTGCAAAAGTTTCTTCTCTCCTCTCTCTCTCTCTCTCTCTCTCTCT
CTCTCTTTCTCTCTCTTTTAAAAAAACATCTGGCCAGGGCACAGTGGCTCAGCGCTGTAATC
CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGCGGAGTTTCGAGACCAAGCCTG
GCCAACTTGGTGAACCCCGCTCTCTACTAAAAATACAAAAATAGCTGGGCATGGTGGCAGG
CGCCTGTAATCTTACTTCTTGGGAAGCTGAGGCAGGAGAAATCACTTGAACCTGGGAGACGG
AGGTTGCACTGAGCCCAAGATCACACCATTTGCGCCAGCCTGGGCAACAAAGCGAGACTCCA
TCTCAAAAAAAATCTTCCAAATGGGTGGGTGTCTGTAATCCAGCACTTTGGGAGGCTA
AGGTGGGTGGATTGCTTGTAGCCAGGAGTTTCGAGACCAAGCCTGGGCAACATGGTGAACCC
ATCTCTACAAAAATACAAAAATAGCTGGGCTTGGTGGTGTGTGCTCTGTAGTCCAGCTGT
CAGACATTTAAACCCAGAGCACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC
TACTGGGCTGCACTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGTCCG
TACAAGATACAGGTCAAAGACTTTGCTGATAAAACAGATTGCAAGTAAAGAGAACCAACCA
ATCCCAACAAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCTGCTCCTCACTGTCTACCTCT
GACAGCATGATGACAGTTTACAAATGCCATGGCAACTCAGGAAGTTACCCGATATGTCCCA
AAAGGGGAGGAATGAATAATCCACCCCTTGTGTAGCAAAATAAGCAAGAAATAACCAATAAA
GTGGGCAACAGCAGCTCTAGGCGCTGCTCTGTCTATGGAGTAGCCATTCTTTTGTTCCTT
TACTTTCTTAATAAATTTGCTTTACCTTAAAAAAA

FIGURE 93

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002
><subunit 1 of 1, 544 aa, 1 stop
><MW: 60268, pI: 9.53, NX(S/T): 3
MLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYWFK
AVTETTKGAPVATNNHQGREVEMSTRGRFQLTGDPKAGNCSLVIRDAQMQDESQYFFRVERGS
YVTYNFMNDGFFLKVTVLSTFPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLCAADSQPPATLSWVLQNRVLSSSPWPWGPRL
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSQSPSDPGVLELPRVQVEHEGEFTCHARHP
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP
KSSTQAPESQESQEBELHYATLNFPGVRRPRPEARMPKGTDQADYAEVKFQ

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

0978375-104501

FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAGAGTCAACGCAATGAACTGTTATTATTACTGCTGCGTTT
TATGTTGGGAATTCCTCTCCTATGGCCTTGCTCTGGAGCAACAGAAAACCTCTCAAAACAAAGA
AAGTCAAGCAGCCAGTGCATCTCATTTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
TTTGTACCGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTTAGA
CAATGGAAACAATTCCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGCGAGTCCCTC
TACATCTTAAGAGCCGAGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
GTTTGTCTCATCAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG
AGGCCATTGTACAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
GCTGACGATCCCTCAAGTGGTAAATAGTCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
ATATTTTCTGTTGAACCAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC
TGCAAGATGAGTATTGGGTAAATCATTCAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
TCTGGAAACAACAAGTGATTAATTAACCTTTCAGATGTTAATGACAATAAGCCTATATTTAA
AGAAAAGTTATACCGCTTGACTGTCTCGAATCTGCACCCACTGGGACTTCTATAGGAACAA
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTTGAAGAGGAT
GATTGCGAAACATTGGACATTTATCTAATCATGAACACTCAAGAGGAATAGTTTATTTAAA
AAAGAAAGTGGATTTTGAGCACCAGAACCACTACGGTATTAGAGCAAAAAGTTAAAAACCATC
ATGTTTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAAGATCCAG
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGATTTTGAAGTTTTTGA
AGAAAACCCACAGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCAGACATAGGAAAT
CTCCTATCAGGTATTCTGTTACTAGGAGCAAAAGTGTCAATATCAATGATAATGGTACAATC
ACTACAAGTAACCTCTGATTGCGTGAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAAACATCA
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAAGGCTCT
GGTCAGGTAAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT
TTACTTTAATCTATCTGTAGAAGACATAACAATTCAGTTTTACAATCATAGATAATCAAG
ATAACACAGCTGTCAATTTGACTAATAGAACTGGTTTAAACCTTCAAGAAGAACCTGTCTTC
TACATCTCCATCTTAATTTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCCTTAC
CATCCATCTGTGATGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACAGGAGCTTG
TGCTTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTGCATTATGATCATA
TTTGGGTTTATTTTTTGACTTTGGGTTTAAACCAACGGAGAAAACAGATTCTATTTCCTGA
GAAAAGTGAAGATTTTCAGAGAGAATATATCCAAATATGATGATGAAGGGGGTGGAGAAGAAG
ATACAGAGGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
CGGAAAACCAACAGCGCTGAGATCAGGAGCCTATACAGGCACTTTTGCAGTTTGGCCCGCA
CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTTAATACGATCCGTGTG
CCCCCTCTTTGATTCCCTCCAGACCTACGCTTTTGGAGGAACAGGGTCATTAGCTGGATCC
CTGAGCTCTTTAGAATCAGCAGTCTCTGATCAGGATGAAGCTATGATTACCTTAATGAGTT
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAGG
GCTTTTTTACCATCAAAATTTTTAAAAGTGCTAATGTGATTTCGAACCCAAATGGTAGTCTTAA
AGAGTTTGTGCCCTGGCTCTATGGCGGGAAAGCCCTAGCTATGGAGTTTCTGATTTCC
CTGGAGTAATACTCCATGTTATTTTAAAGTACCTACATGCTGTGATTGAACAGAGATGTG
GGGAGAAATGTAAACATCAGCTCACAGGCATCAATACAACCAAGATTGGAATGAATAATG
TAGGAAGATATTTAAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT
CAATTTTACTTAGGAAAGAGTAAAAATACCAACGAGAAAAATTTAAGGAGCAAAAATTTG
CAGGTCAAATAGAAAATGTACAAATCGAGATAACATTTTACATTTCTCATATTGACATGAAA
ATTGAAAATGTATAGTCAGAGAAAATTTTCATGAATTTTCCATGAAGTATTGTTTCTTTAT
TTAA

FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLWPCLGATENSQTKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH
IGQLRSDLNDGNNSFYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVSINDINEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL
LYSLLQGQPYFSVEPTTGIVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPTGTSTIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIIITNHE
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDRISA
WYNSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVDCDGSSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIHQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGLAGSLSSLESASVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

0978375-101604

FIGURE 96

ATTTC AAGCCAGCCATATTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
AGCATTGAAGAGGATGATTCGCAAACATTTGACATTATT

05978375.101601

FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCCGAC
CCAGAGCTTCTCCAGCGGCGGCGCAGCGAGCAGGGCTCCCCGCCTTAACCTCCCTCCGCGGGG
CCGAGCCACCTTCGGGAGTCCGGGTTGCCACCTGCAAACTCTCCGCTCTCGCACCTTGCCA
CCCCGTGAGCCAGCGCGGGGCCCGAGCGAGTCAATGGCCAACGCGGGGCTGCAGCTGTTGGGG
TTCATTCTCGCTTCTCTGGGATGGATCGGCCCATCGTCAGCACTGCCCTGCCCTAGTGGAG
GATTTATCTCCATGCGCGGCACAAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGA
TGTCTCGGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT
CTGAGCAGACATTGCAAGCAACCCGTGCTTGTATGGTGGTGGCATCCTCTGGGAGTGAT
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGAAGACGATGAGGTGC
AGAAGATGAGGATGGCTGTCAATGGGGGTGCGATATTTCTTCTTGCAGGTCTGGCTATTTTA
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCATGACCCCTATGACCCGAGT
CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCTACTGGCTGGGCTGCTGCTTCTCTGCCC
TTCTGGGAGGTGCCCTACTTTGTCTGTTCTGTCCCGAAAAACAACCTTTTACCACAACCA
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGACACAGAGGCCAAAG
GAGAAATCATCTGTAAACAACCGAAAATGGACATTGAGATACTATCATTAAACATTAGGAC
CTTAGAATTTTGGGTATGTGTAATCTGAAGTATGGTATTACAAAACAACCAACAAAACAAA
ACCCATGTGTTAAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTATCTTCTTCTCTCA
ATATAGGAGGGGAAGATTTTTTCCATTGTATTACTGCTTCCCATTTGAGTAATCATACTCAAAT
GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGATATATACATGTTTTTCTTATTA
ATAGACAGTAAATACTATTCTCATTATGTTGATAGTACATAGTAAATATCTCTAAAT
AGGTAATGTATTTAATCCATATTGATGAAGATGTTTATGGTATATTTCTTTTTTCGTC
TTATATACATATGTAACAGTCAAATATCATTACTCTTCTTATTAGCTTTGGGTGCTTTG
CCACAAGACCTAGCCTAATTTACCAAGGATGAATTTCTTCAAATCTTTCATGCGTGCCTTTT
CATATACCTATTTTTATTTTTTACCATAATCTTATAGCACTTGCACTCGTTATTAAGCCCTTAT
TTGTTTTGTGTTTTATTGGTCTCTATCTCTGAACTAACACATTTTCATAGCCTACATTTTA
GTTTTCTAAAGCCAAGAAATTTTATTACAAATCAGAACTTTGGAGGCAAAATCTTTCTGCACT
ACCAAAGTGATAAAATTCCTGTTGACCTTCCCAACAATCCCTGTACTCTGACCCCATAGCAGT
CTTGTTTGTCTTTGAAAAATTTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTGT
AACACAACCTTTATGATTGAATTTTTAAGCTACTTATTTCATAGTTTTATATCCCCCTAACT
ACCTTTTTGTTGCCATTCCTTAATTGATTTGTTTTCCCAAGTGTAATTTATCATGCGTTTTTA
TATCTTCTTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA
ATCTGGTGACAAATATCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTACCTCTTTT
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAAGTTAGAAGAGGTAGTGTGAATATTAA
TTAGTTTTATTTACTCTTATTTTGAACATGAACATATGCCATGTAGTGTCTTTATTTGCT
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAACCTACACAGCTACCTTCATGTGATT
CACTGCTTCTCTCTACACAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCAT
GTGGTTCAGTGCTTCTCTCTTACCAGTCTATTTCCACTGAACAAAACCTACGACATATC
CTTCATGTGGCTGCGCTTCTCTCTTACCAGTCTATTTCCATTCTTTTCAGCTGTGTCT
GACATGTTTGTGCTCTGTTCCATTTTAAACAACCTGCTCTTACTTTTCCAGTCTGTACAGAATG
CTATTTCACTTGACAGATGATGTAATGGAAGGGTGTGGCACTGGTGTCTGAGACCTG
GATTTGAGTCTTGGTGTATCAATCACCGTCTGTGTTTGAAGCAAGGCATTTGGCTGCTGTAA
GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCACCTCACAGTGATG
TTGGGGGATCAGTGAGATAGAATACATGTAAGTGTGTTTTGTAAATTTAAAAAGTGCTAT
ACTAAGGGAAGAATTGAGGAATTAACGTACATCGTTTTGGTGTGCTTTTCAAATGTTTGA
AAATAAAAAAATGTTAAG

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0007035-101601

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185
```

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFILAFGLGWIGAIIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTQOI
QCKVFDSSLNLSSTLQATRALMVVGILLGVIAIFVATVGMCKMCKLEDDDEVQKMRMAVIGGA
IFLLAGLAILVATAWYGNRIVQEFYDPMTPVNARYEFGQALFTGWAAASLCLLGGALLCCSC
PRKTSYTPRPPYKPPAPSSGKDYV

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC
GCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAAN
CNTTCAACANTTCTATGACCCCTATGACCCCAAGTCAATGCCAGGTACGAATTTGGTCA
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCT
GTTCTGTCCC

09978375.101601

FIGURE 100

ACCCCTTGACCCAACGCGGCCCGACCGNNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG
GCTTCATTCTCCCCTTCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT
GAATCTGAGCAGCAATGTGAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGGAAGACGATGA
GGTGCAAGAAGATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTTCTTGCAGGTCTGGCTA
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCATGACCGA

00978375.101601

FIGURE 101

GGGCCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANACCGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTT
CTTGCAAGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAGAAT
TCTATGACCCATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTCTGCTTCTGGGAGGTGCCCTACTTTGCTGTTCTGCGA

0070375-10101

FIGURE 102

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT
GCNTGTGCGAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGAAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTCAATGGGGGCGCGATATTTCTTGTTGCAGGCTCTGGCTATTTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCCTATGACCCCGTCAATG
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG
GGAGGTGCCCTACTTTGCTGTTCCCTGTCCC

00070375-101001

FIGURE 103

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC
AAGCAACCCCTTGCCCTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGACAGGTCTGGCTATTTAGTNCCACAGCAT
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCAGTCAATGCCAGGTAC
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCCTTCTGGGAGGTGC
CCTACTTTGCTGTTCTGTCCCCGAA

09078375-101601

FIGURE 104

AGCAATGCCCTGCCCCAGTGGAGGATTAATTCCTATGNTGGGACAAACATTGTGACNGCCC
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTGSCAGAGCACCGGGCAGATCCAGTGC
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTGTGGCCACCGTGGNAATGAAGTGATGA
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATGGGGGCGCGATATTT
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA
ATTTTATGACCCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCCTTNTTCACTG
GCTGGGCTGCTGCTTNTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTCTGCGAACC

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FIGURE 105

TCATAGGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA
TGGCAATAGAATCGTTCAGAATTNTATGACCCTATGACCCAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA
CTTGCTGTTCTG

0978375.101601

FIGURE 106

TTCCTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG
CCACCGTTGGCATGAAAGTGATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGACAGGTCTGGCTATTTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCAGTCAATGCCAGGTA
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTG
CCCTACTTTGCTGTTCTCTGTCCCCGAAAAACAACCTCTTACCCACG

0975375-141604

FIGURE 107

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA
TGTACGAGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNATGCGCTTGATGGTGGTTGGCA
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGATGAAGTGCTTG
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTTCTTGC
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT
GACCCATATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGG
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCTGCGAA

00070375-104604

FIGURE 108

GGGTGCCGTGAGCTCGCCGGGCACCGCGGCTCGCCCTCGCCCTCGGCCCTGCGCCCTGCGCCTGCAC
CCGCTAGACCGACCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCCCGCCGTGCCCCG
ACCGGTCCCCGCCTTTTGTAAAACTTAAAGCGGGCGCAGCATTAACGCTTCCCGCCCGGT
GACCTCTCAGGGGTCTCCCGGCCAAAGGTGCTCCGCCGCTAAGGAACATGGCGAAGGTGGAG
CAGGTCTGAGCCTCGAGCCGCGCAGCAGAGCTCAAATTCGAGGTCCCTTACCAGATGTTGT
CACCACCAACCTAAAGCTTGGCAACCGACAGACCGAAATGTGTGTTTAAAGGTGAAGACTA
CAGCACCAGCTAGGTACTGTGTAGGGCCCAACAGCGGAATCATCGATGCAGGGGCCCTCAATT
AATGTATCTGTGATGTTACAGCCTTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT
TATGGTTTCACTATGTTTGTCTCCAAGTACACTTCAGATATGGAAGCAGTATGGAAGGAGG
CAAACCGGAAGACCTTATGGATTCAAACCTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT
GATAAACCATGATGTAGAAAATAAATAAAATTATATCCACAACATGCATCAAAGACAGAAAC
ACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATAG
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAAGGCTACGGGAGGAGAACAAAGCAGTTCAAG
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTCAAGCATTAGC
CCCAACTGGGAAGGAAGAAGGCCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTTCTTTA
TCGTTGGTGTAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATGCACAGGATGGTAAATTG
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT
AATGTATGATGACATCTCAGAGTCTTGCCCTTAAATTAACCCCTCCCTGCACACACATACAC
AGATACACACACAAATATAATGTAACGATCTTTAGAAAAGTTAAAAATGTATAGTAACTG
ATTGAGGGGGAAAAAGAAATGATCTTTAATTAATGACAAGGGAAACCATGAGTAATGCCACAAT
GGCATATTGTAATGTCAATTTTAAACATTTGGTAGGCCTTGGTACATGATGCTGGATTACCTC
TCTTAAATGACACCTTCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCAGCAT
GCTGGGGAGTGGCTCAGCTCCACACAGTAGTCCCACGCTGGCCCATCCCGGCCAGGCTG
CTTTCCGTCTTCAAGTCTGTTCCAAGCCATCAGTCCCTGGGACTGATGAACAGAGTCAGA
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT
TGACTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA
GCTAAATTTGTATTGGTTCACTGATGAGTCAAAGTCAAACTGTTATTAGAGATGTTTAAATGCATA
TTTAACTTATTTAATGTATTTTCACTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGC
TGCGTGCTGCTGAACTCTGTGGGTGAACTGGTATTGCTGCTGGAGGCTGTGGGCTCCTCT
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA
GGAAGTGTTTTTCTGGGTCACTAAATAACAACCTGTATAGGGAGGGAATTTCTCAGTAGTG
ACAGTCAACTCTAGGTTACCTTTTTAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTTATA
CCACCTCTCAACCATTTACTCACACTTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC
TTGGGGACCTAGCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGCG
ACCAGCAGTTGTGGGTGGGAGCAAGGGAAGAGAGAACTCTCAGCGAATCCTCTAGTAC
TAGTTGAGAGTTTGACTGTGAATTAATTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA
CTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCCCCAAAAATTAGAAAA

FIGURE 109

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977
<subunit 1 of 1, 243 aa, 1 stop
<MW: 27228, pI: 7.43, NX(S/T): 2
MAKVEQVLSLEPQHCLKFRGPFTDVVTTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID
AGASINVSVMQLQPFDDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRGVFE
LPAENDKPHDVEINKIIISTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE
NKQFKEEDGLRMRKTQVQNSPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

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FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCCTGCGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCC
CCAAAATTAAGAATTCTTTTGTCATTTGTGCACATTTGCTCTATGGGGGAATTATTATTTT
ATCATTTTTATTATTTTGCCATTGGAAGGTAACTTTAAATGAGC

09/03/5, 101601

FIGURE 111

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG
GGGAGTGCGGTGAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTGCTTT
CCGTGTCITTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT
AAATTGTATTGGTTCATGTAGTGAAGTCAAACGTGTTATTCAGAGATGTTTAATGCATATTTA
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTGACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAACCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

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FIGURE 112

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG
AAAGTTAAAAATGTATAGTAAC

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FIGURE 113

GGTGGCCCATTCCTCGGCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACGTGGCAGCATNAGACGTAC
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTGGAAATAAATGGCAGT
GCTTTGTTCAANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACG
TTATTCAGAGATGTTTAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

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FIGURE 114

TGCTTTCCGTGTCCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTA CTGTCATAAGTGAGAGGCGTG
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGTCTTATTAGAGATGTTTAATGC
ATATTTAACTTATTTAATGTATTTCATCTCATGTTTCTTATTGTCACAAGAGTACAGTTAA
TGCTGCGTGC

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FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTTATTAATGACAAGGGAAACNTGNGT
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC
TGGATTACCTCTCTTAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANCCCC
GGCCCAGGCTGCTTTCCGTGTCTTCAGTTCGTCCAAGCCATCAGCTCCTTGGGANTGATGA
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCANTT
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTCAGAGATG
TTTAATGCATATTTAANTTATTTAATGTATTTTCATNTCATGTTTTCTTATTGTCAACAAGGGT
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC
CACGTGGCCCACTCCCGGCCCAGGCTGCTTCCGTGTCITTCAGTTCTGTCCAAGCCATCAGC
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCAC TGTGGCAGCATCAGACG
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC
AGTGCTTTGTTCAC TTAAAGGGACCAAGCTAAATTTGTATTGGTTTCATGTAGTGAAGTCAAA
CTGTTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTC
TTATTGT CACAAGAGTACAGTTAATGCTGCGTGCTGCTGAAC TCTGTTGGGTGAACTGGTAT
TGCTGCTGGAGGGCTGTGGGCTCCTCTGCTCTGAGAGTCTGGTCATGTGGAGGTGGG

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FIGURE 117

GCGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA
 GGCTCCCAGCTGTCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC
 CTCGGGGACCAACAAGCCTGGCAGGGTCTCATTGTGTGCCAGGCTGGAGTTTCAGTGCCA
 TGATCATGGTTTACTGTCAGCCTTGACCTCCTGGGTTCGAAGCGATCCTGCTGAGTAGCTGGGA
 CTACAGGACAAAAATTAGAAGATCAAAATGGAAAAATATGCTGCTTTGGTTGATATTTTTACC
 CCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA
 GGTACCCCGGATTGTGAGTGAAAGGACTTTCCATCTCACCAGCCCCGATTTTGAGGCAGATG
 CTAAGATGATGGTAAATAAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCGAGC
 CTTTCTGAATTGGAGGATTATCTTTTCCATGAGACTGTCTTTGAGAATGGCACCCGAACCTT
 AACGAGGTGAAAGTTCAAGATTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG
 TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCGTTTCAGCATCTTGGACAAA
 AGGTTCTTAACCAATTTCCCTTTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT
 TCTCATTTCCTCTCAGCATGTTCTAACTGCTGCCCACTGTGTTTCATGATGGAAGGACTATG
 TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG
 AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAAGAGAGGGGTAC
 CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAGAAGAAAGAAATCTGGCGGGGTCT
 AGAGGATTGCCGAAGGGAGGCCCTTCCTTTTCAGTGGGACCCGGGTCAAGAATACCCACATTCGG
 AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGCATATGACTATGCTCTTCTGGA
 GCTGAAGCGTGTCTCAAAAAAGAAATACATGGAACCTTGGAAATCAGCCCCACGATCAAGAAAA
 TGCTGTGGTGAATGATCCACTTCTCAGGATTGTGATAACGATAGGGCTGATCAGTTGGTCTAT
 CGGTTTTGCAGTGTGTCGACGAATCCAAATGATCTCCTTTACCAATACTCGCATGCTGAGTC
 GGGCTCCACCGGTTTCGGGGGTCTATCTGCGCTGAAAGATCCAGACAAAAAGAAATTGGAAGC
 GCAAAATCATTGCGGTCTACTCAGGGCACAGTCAGGTGGTGGATGTCCACGGGGTTTCAGAAAGAC
 TACAACGTTGCTGTTTCGCATCACTCCCCTAAAAATACGCCAGATTTCGCTCTGGATTTCACGG
 GAACGATGCCAATTGTGCTTACGGCTTAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA
 TCACAGAGAAAAACGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCTCGGACTT
 GAACCTCTGTCAATAGCATTTCAACATTTTCAAAATCAGGAGATTTTCGTCCATTAAAAAAA
 TGTATAGGTGCAGATATTGAAACTAGGTGGGCACCTTCAATGCCAAGTATATACTCTCTTTA
 CATGGTGATGAGTTTCATTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTT
 AAACCTTCAAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC
 TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA
 GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA
 CTCGTGAGATGGATCCATTTCAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT
 GGGACATTAGTTAGTTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATAAA
 CAAAATAAAGCTGTTTTTACTGCTTTTAAAGAAATAACAATTCAAGTGTGATATTATTTAAAAA
 TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTGAAGAAAGGGAAGCTGAGACATT
 TAAGATCTCAAGTTTTTATTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG
 AAGACATTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT
 TCTATGTATAGGTGCTACATTTTATAGGACAAAGAATTCTGTAATCTTTTCAAGAAAGAGT
 CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGTGAATTCTCTGATTAG
 TAATTTTATAGATGCTCTTCTTCAAAATGAATAAAATTTATGAATATGA

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FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253
<subunit 1 of 1, 413 aa, 1 stop
<MW: 47070, pI: 9.92, NX(S/T): 3
MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC
GIECQKELPTPSLSLELYSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV
YGTDSRFSILDKRFLTNFFPSTAVKLSTGCSGILISPQHVLTAAHCVHDGKDYVKGSKKLRV
GLLKMNRKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGMGMDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCVSVSDSNLLYQYCDAESGSTGSGVYLRLLKDPDKKNWKRKIIAVYSG
HQWVDVHGVQKDYNAVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

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FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTAGTGTCCGATTCTGATTCCGGCAAGG
ATCCAAGCATGAATGCTGCCGTGGGCAACTCTGGCACACTGCTCCTCTTTCTGGCTTTC
CTGCTCCTGAGTTCAGGACCGCACGCTCCGAGGAGGACCGGACGGCCTATGGGATGCGCTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCTCCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCACCAGAAGCAGGTGATTTCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCTGACAACCCATGTTCACTCA
AGTGCCAAGCAAAGGAACAACCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAATCGGATGATACT
GTGGTTGCACTTCCTATGGAAGTAGACATATTGCGCTTGCTTAAAGGTCTGATCACTT
ATATCTGGAACCAAAACCTCCAGGGGACTAAAGGTGAAAAAGTCTCAGCTCCACAGGAA
CTTTCCTTGTTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAGAGATACTGAGA
ATGGCTGGACCACCTCACAGCAGATTTCAATGTCAAGATTGTAACCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGTTATCAGCTGACATCGGCTGAGTGTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCCCTCCTCGGTGGGAGGCCACCCATGGACCGCGTGCTCCTCC
TCGTGTGGGGGGGCGATCCAGAGCCGGGCAGTTTCTGTGTGGAGGAGGACATCCAGGGGCA
TGTCACTTCAGTGAAGAGTGGAAATGCATGTACACCCCTAAGATGCCATCGCGCAGCCCT
GCAACATTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGTCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA
AACCCAAAGAGAACTTCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGTGTGTGTGTCAGAGGAGCCCTCGTAAAGTTGTAAAAGCACAGACTGTTCTATA
TTTGAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTTATGGTTCTGA
ACTAAGTGTAACTCATCTCACCAAGCTTTTTGGCTCTCAAATTAAGATTGATTAGTTTCAA
AAAAAAAAA

0978375.101601

FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLLFLAFLLLSSRTARSEEDRDGLWDAGPWPWSECRTCGGGASYSLRRCLS
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPCLKQC
AKGTTLVVELAPKVLDTGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDHLYLETKTLQGTKGENSLSSSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFPPCS
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQCNI
FDCPKWLAQEWSPCTVTTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLPVEAKLPWFKQAQELEGA AVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

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1095075570660

FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACCTCCCGTGGAGGGGCCCGTGGGCCCTCGGGCCTGAC
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGCGCTGTGGCTGGCG
GCCCGCCGGTTCGTGGGGCCAGGGTCCAGCGGTGCGCAGAGGCGGGGACCCCGGCCCTCAT
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCCG
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCCGAGGAG
GCGGCGGGTCAGCTCCGCGCGGAGCTCCGCCAGGCCGCGGAGTGCGGCCACAGAGCCTGGCGT
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG
CCTTCTGCCAGGAAATGCTCCAGGAAGACCTAGGCTGGATGTCTTGATCAATAACGCAGGG
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA
TCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCTCAAAAGTTTCAGCTCCAGCA
GGATTGTGGTAGTTTCTTCCAAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC
AGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAACTGGCTAACATTCTTTT
TACCAGGGAAGTAGCCCGCGCTTAGAAGGCACAAATGTACCGTCAATGTGTTCATCCTG
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC
AATTGTGTGTATGGGCTTTTTCAAAACCTCCAGTAGAAGGTGCCCAGACTTCATTTATTT
GGCCTCTTCACCTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGGGGATTGTAAAGAGGAAG
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCTGGGATATCAGTGAAGTG
ATGGTTGGCCTGCTAAAAAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAG
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTACTTGAAGAAAAGAATTTTG
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATATTTT
TGGGATAAGAGAATTTGAGCAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA
GTACAAATGAAAAATACAATTATATTGTAATAATATAACTGGGCAAGCATGGATGACATATTA
ATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTTTGTGTGGAATTAATCTGC
CTGGTGTGTGCACACAAGTCTTACTTGAATAAAATTTACTGGTAC

FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEAAAGQLRREL RQAAECGPEPGVSGVGELIVRELDLASLSVRA
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHIGHFLLTNLLGLLKSSAPSR
IVVVS SKLYKYGDINFDDLNSEQSYNKSFCYSR SKLANILFTRELARLEGNTVTVNLHPG
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE
LLPKAMDESVARKLWDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

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FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAAGTTGTTACT
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG
TTACTGAAAAATTATTTTGGGATAAGAGAATTTTCAGCAAAGATGTTTTAAATATATATAGT
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA
AGCATGGATGACATATTAATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTACTACAATGTTTGGTGTT
TGTGTGGAAATTATCTGCCTGGCTT

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FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGAGCCCAGCC
CTTTCTTAACCCAAACCAACCTAGCCAGTCCCAGCCGACGCGCTGTCCCTGTACAGGAC
CCCAGCGTTACCATGCATCCTGCCGTCTTCTATCCTTACCCGACCTCAGATGCTCCCTTCT
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACGTAAATAACAAGTCTTGCTACAGAGA
ATATAGATGAAATTTTAAACAATGCTGATGTTTGCTTTAGTAAATTTTATGCTGACTGGTGT
CGTTTCAGTCAGATGTTGCATCCAATTTTGGAGGAAGCTTCCGATGTCAATTAAGGAAGAATT
TCCAAATGAAATCAAGTAGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC
AGAGATACAGGATAAGCAAAATACCCAACCTCAAATTGTTTCGTAATGGGATGATGATGAAG
AGAGAATACAGGGGTGAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAG
TGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAA
ATATCATTGGATATTTTGAGCAAAAGGACTCGGACAACTATAGAGTTTTTGAACGAGTAGCG
AATATTTTGCATGATGACTGTGCCTTCTTTCTGCATTTGGGGATGTTTCAAACCCGAAAG
ATATAGTGGCGACAACATAATCTACAAACCACCAGGCATTCTGCTCCGATATGGTGTACT
TGGGAGCTATGACAAATTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTT
GTCCGAGAAATAACATTTGAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGC
AATTAATAAGTAAAAAGGTACAATAAACTTTTACATGCCGATTGTGACAAATTTAGACAT
CCTCTTCTGCACATACAGAAACTCCAGCAGATTGTCTGTAAATCGCTATTGACAGCTTTAG
GCATATGTATGTGTTTGAGACTTCAAAGATGTATTAATTCCTGGAAAACTCAAGCAATTCG
TATTTGACTTACATTCTGGAAAACTGCACAGAGAATTCATCATGGACCTGACCCAACTGAT
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAA~~AA~~AACTTG
AAAAACAGTTTGTAAAGCCTTCAACAGCAGCATCAACCTACGTGGTGAAATAGTAAACCTA
TATTTTCATAATCTATGTGATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 125

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46927, pI: 5.21, NX(S/T): 0
MHPAVFLSLPDLRCSLLLLVTWVFTPTTETITSLATENIDEILNNADVALVNFYADWCRFSQ
MLHPIFEEASDVIKEEFPNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKEYR
GQRSVKALADYIRQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKDSDNRYRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI
TFENGEEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPESSFQKLAPSEYRYTLRLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

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FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCCTCAAATTGTTTCGTAATG
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

09978375.101601

FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCGCCGCNCGAGCCCGGGTCGAGAGGACNAGG
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGAGCCAGCCCTTTCCTAACCC
AACCACCTAGCCCNGTCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCAGCGTNACC
ATGCATCCTGCCGCTTCTCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC
TTGGGTTTTTACTCCTGTAACAACCTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTGCGTTTCAGTCAG
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA
TAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

0978375-101601

FIGURE 128

CCCCACGCGTCCGATGGCGTTACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCGCGCTCATCTTCTTCGCCATTGCGCACATTATAGCATTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGAATACCCCTGAATCCCCCTTGACTCCCAGAGTACCTCAT
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCCCTCTTGGCATATCATATTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCAGGA
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTGAGAAGGAAGGATG
GTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTACTACCTATATGGCATGATCTATGTTT
TGGTGAGCTCTTAGAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTGCTTGTGGAAAGACTG
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT
GATTACCTCTGGTGTGACAGGTTTGAACCTTGCACTTCTTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCTAGTACATTGGAAGCTTTTGTTTATAGGAACCTGTGA
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAAAATGTATATCTGACTAGTGGGAAACTTCATGGGTTTCTCATCTGTCT
ATGTCGATGATTATATATGGATACATTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTCCCATATTTCCATCAGAGTAATAAA
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAAATTGCAGG
TACTACAGATTTTCAAACCTGAATGAGAGAAAATGTATAACCATCTGCTGTTCTTTAGT
GCAATACAATAAACTCTGAAATTAAGACTC

09978375.101601

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

0978375-101601

FIGURE 130

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCCTG
AATCCCCTTGTTACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCTCTTGGCATATCATATTTGGAGGTATA
TGAGTAGACCAGTGATGAGTGGCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACAGAAGAATT
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

0978375-101601

FIGURE 131

CGGACGCGTGGGGAAACCCCTCCGAGAAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAAACAAGATGGCGCGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCGCGCCG
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTTCGGGGACCGCTTCGGCTGAAGCATTTGAC
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACAC
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTGTG
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGAATGTGAATCTGCATGTACA
GAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC
ATTGCTGAACCTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAATAAGTTATATTCCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA
GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA
GAAAGTGATGGCTTTTTAAGATGCCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCT
TGTCCTCTCGGTGATGGTATTGCTTTGGATTGTGTGCAACTGTTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAAAGTGAAGATCATGAAGA
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAATTTCCACTCCTCATAGAGCTTTTAAATGGTTTCA
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAATAAAGTTACTCAAATCTGTG

09978375.104604

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGS LWVRTQLGLPPLLLLTALAGSGTASAEAFDSVLGDTASCHRAQQLTYPLHTYP
KEEELYACQRGCR LFSICQFVDDGIDLNR TKLECESACTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQLMSLMPKMHL LFP LTLVRSFWSDMMDSAQSFITSSWTFY LQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSY LQMRNSQAHRNFLEDGESDGF LRC LSLNSGWILTTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

09078375.101601

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTTCGC
TGAACCTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTCTCTAA
CTCTGGTGAGGTCAATCTGGAGTGACATGATGGACTCCGC

0978375.101601

FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA
GCTGAGCTGCTGTGACAGAGGGAAACAAGATGGCGGCCCGAAGGGAGCCTTTGGGTGAGGAC
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGCCCGAGGTTCTGGGGACCG
CTTCGGCTGAAGCATTGTACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTGAC
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTGAGAGAGTTG
CAGGCTGTTTTCAATTTGTGAGTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT
GGTTGCCAGAATCAGCTGCCATTCGCTGAACTGAGACAAGAACTTATGTCCCTGATGCC
AAAAATGCACCTACTCTTTCCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT
CCGC

0073375-101601

FIGURE 135

GCAGAGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCTGGGAGGCGGCCCGGAGGT
GGGGCGCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCAGCCGAGC
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGAGAGCTGCAATGGGGCCGCGGCTG
GGGATTCCTGTGTTGGCCCTCTGGGCGCCGTGTGGTGCTCAGCTCGGGCCACGGAGAGGAGC
AGCCCCCGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT
ACCTGTGATGTTGAAACCATTGTAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCTTTCT
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA
GTTCTGATGGAATTAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCCTCAGATAACTTCTGTGAAGCTGATGAC
ATTCAGTCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA
CAAGGGACCGATGCTTGGAAAAATATGGAATGTCTACGAAGAAAACTGTTTTAAGCCAC
AGACAATTAAGAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGG
CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTACAAGAGACCTGGTTAG
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA
GGAGAAGGTCCAAGAAGGCTTAAGAACTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT
ATCCAAAGTGTTACCATTCCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAATAAAATTC
AGGATGAGGAAAAAAAATGTTACTTCTGGAATACTTCATGAAATCAAGTCATTTCCTTTG
CATTTTGATGAGAAATTCATTTTTTGCTGGGGATAAAAAAGAAGCACAAACTAAAGGAGGA
CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG
AAATTGATAGCAAAATATGCCAGAAAGTGGACCTAGTTATGAATTCATCTAACGAGACAAGA
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAGAATTAGAAAACT
TCAGGAAGCTGTTACAGAATATTCATTAAAGAAAAACAAGCTGATATGTGCTGTTTCTGGAC
AATGGAGCGCAAGAGTGGAAATTCATTCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA
ACATTTTATATAAAGTGTCTTTTGTAAAGGAGAAATATATTTGTTTAAAGTAAACACATTTT
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAAGTAATACTTTAATAATGTG
GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 136

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974

<subunit 1 of 1, 468 aa, 1 stop

<MW: 54393, pI: 5.63, NX(S/T): 2

MGRGWGFLFGLLAGAVWLLSSGHGEEQPPETAARCFQCQVSGYLDCTCDVETIDRFNNYRLF
PRLQKLLESDFRYRYKVNLRKPCFFWNDISQCGRRDCAVKPCQSDEVPDGIKSASYKYSEEA
NNLIEECEQAERLGAVDESLSSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNP
RYTYGKGPDAWKIWNVIYBENCFFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI
ELRALSQVLPFFERPDFQLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH
KLKEDFRLHFRNISRIMDCVGCFCRLWGLQTQGLGTALKILFSEKLIANMPESGSPSYEFH
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 280-283 and 384-387

Amidation site.

amino acids 94-97

Glycosaminoglycan attachment site.

amino acids 20-23 and 223-226

Aminotransferases class-V pyridoxal-phosphate

amino acids 216-222

Interleukin-7 proteins

amino acids 338-343

0978375.101601

FIGURE 137

GCTGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACATTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA
ACATTACAGAATTTNACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT
CTTNGAGCGCCAGATTTTCAACTNTTTACTGGAATAAAAATTCAGGATGAGGNAAACAAAA
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTTCTTTGCATTTTGATGAGAATTCA
TTTTTTTGCTG

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FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGCAGGATGGGAGGGAA
AGTGAAGAAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC
CGATCAGGCATGGAACTCCCCCTTCGTCACTACCTGTTCTTGCCCCCTGGTGTTCCTGACAGG
TCTCTGCTCCCCCTTTAACTTGGATGAACATCACCCACGCTATTCCAGGGCCACCAGAAAG
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG
GGCCCCAATATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCTCTC
ATCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTCT
ATGGTGAGCTTAAAGGAGAGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA
GTGTGGTAAGGGAAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCTAGAAAGCAAA
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT
GCCCTCCCAAGCCTGGGAGTAACATATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCT
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGGATGCTTCATTCCA
GCCTCAGGGAAGCCTGGCACCCACTGCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG
CCTGCATGGCTATCCTCATGTCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCCTAACAGA
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG
GTGGGCAGATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAATCCAT
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTGCGGTG
AGCCAAGATTGTGCCTCTGCACTTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA
AATAATAATAATAATAATTCAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTAAAAAT

0978375.101601

FIGURE 139

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13352, pI: 5.99, NX(S/T): 1
MELPFVTHLFLPLVFLTGLCS PFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW
DGPSGDRRGDVYRCFVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

09978375-101601

FIGURE 140

CACAGTTCCCCACCATCACTCNTCCCATTCCTTCCAACTTTATTTTTAGCTTGCCATTGGGA
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACTCCCTTCGTCACTCACCTGTTCTTG
CCCCTGGTGTTCTTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT
ATTCCCAGGGCCACCAGAAAGCTGAATTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGACGTT
TATCGCTGCCCTGTAGGGGGGGCCCAATGCCCATGTGCCAAGGGCCACTTAGGTGACTA
CCAACTGGGAAATTCACTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA
CAGATGGTGATGG

0978375-301604

FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCTTCGGAGCCCCCTTTCTGAGCTTCTTGGGCCGGCTCTAGAACA
ATTCAGGCTTTCGTGCGACTCAGACCTCAGCTCCAAACATATGCATTTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTTCCATGTTTGTCTACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTGTATGTGGAGCCAGTGATCGCGCTGGAGA
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC
ACGCCACTGTGCCATACAACCTTCGTGTCAAGGCCACATTGGGCTCACAGACCTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
CTTGTGGCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
GGGTATTTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
CATTCTGTGAAGGCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGT
GGTCGTGCCACTGTTCTGTCTGAAAATGGGCCGGCTGCTCCAGTACTCTGTTGCCCGTGG
TGCTCCTCCAGACACCTTGAAAATAACCAATTACCCCCAGAAGTTAATCAGCTGCAGAAGG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCTCAGGGCCTGGAT
CTCATAGGTTTTCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA
TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTGAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGGAGAGCCCCACTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCATTCAAGCCCAATGCCGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGATGAACACGGAGGATC
CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
GTGCAATGCGACGAGAATGCAGAAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
TGTTGGTAAAGTACAGAATTCAGCAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
AAAAA

0978375-101601

[illegible]

<subunit 1 of 1, 311 aa, 1 stop

MQTFTMVLLEEIWTSLSFMWFFYALIPCLLTDEVAILPAPQNLVSLSTNMKHLMLMWSVPVIAIGE
TVVYVSVEYQGEYESLYTSHIWIWPSWSCSLTEGPBCDVDDITATVPYNLRVRATIGKQTSASW
SILKHFPFNRSNLTALTRPKMETIKDGFHLVIELEDLGPQFEFLVAYWRREPGAEHHVQMSRAG
GIPVHLETFMNEPGAAYCVQKAEITVKAIGRYSAFSQTECEVGEAIPVLVLAFAVFGFMILLV
VVPFLVPMKMRLLQYSCCPVVVLDPDLTKITNSPQKLISCRREEVACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation site.

amino acids 40-43 and 134-137

Tissue factor proteins.

amino acids 92-119

Integrins alpha chain proteins

amino acids 232-262

FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGAAAGAAACAATGTTCTAGG
TCAAAC TGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACC AAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGCGAACCCCTTGCGGCGCAAAGGG
GTTNGCGAACCCCTTGCGGCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

00978375-104604

FIGURE 144

CCCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA
GGCAGGAGAGGAGGAGGTGGGGAGAGCAGAACTGGAGGCCGACACTGAGGGAGGGCGGGA
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA
GTAGGAAGATCAGGAGCTAGAGGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG
GCTGCTTTGGCATTGGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCTT
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGCAGGGCGTTGGG
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCTCGAGC
GCTGTTACTCTGGGCTGCACTGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGC
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAAAGCTCAGCACTGGAGGAGAGA
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCT
GTGGTCAATGTGTCTGGAGGTCCCTCCTTTACAGCCACCGACTCAGTGAAGTGGCGTGTCT
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGTCTG
AGGTGCAGCTCATTCACTTCAACCAGGAAGCTTACGGGAATTTAGCGCTGCCTCCCGCGGC
CCCAATGGCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCATTCTCT
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCTCTACAAGAATGATGCCTACTTTC
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACTATCAGGGC
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTCACTTGATCCTCATTGACCGGGCCCTCAA
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT
TCCAGAGCCTCAGCGTAACAGCCGGCCCTGCAGCCCTTGGCCACAGGGCACTGAGGGGC
AACAGGGACCCCGGCACCCCGAGAGCGCTGCCGAGGCCCCAATAACCGCTGCATGTGGA
TGGTGTCCCCCATGGTGCCTGGAGACTCCCTTCGAGGATTGCACCCGCCGTCTAAGCCTC
CCCAAGGCGAGGGGAGTTACCCCTAAACAAGCTATTAAAGGGACAGAATACTTA

0978375.101601

FIGURE 145

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVGPFPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGG EKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL
LYSHRLSELRLLF GARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLS TPPCSE
TVTWILIDRALNITSLQMHSLRLLSQNPSSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER
RCRGPNYRLHVDGVPHGR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 177-199

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

097375, 01604
T09701, S48266

06097

GGCGGCTCGGTTCTCGCGCGCTCGGCTCTGACGGACGAGGACGAGAGCTCGGCCGACCGCTCTCGCGCGCGAGCGCTC
 GTCTGTGTCCTCCCGCCCTCGCTCTCTGTCAGCATCTGCTCTAGAAAGCTCGTGGGGGCCCACTCGTGGCGACATACGAAC
 CGACGCTCCCTTCCACCACCCAGCTCGAGCTCTAATTTTGGACAGCTTTGGCTCTCGATTTTCTCGAGTTGAGGGAGC
 CGACGAGCGAGGCTCGGATTCGCTTCTGCACTGACGACCACGCTCGCCCTCGAGCGCTCGGTGCTCGAGCCCTTC
 CGACGCGGCGCTCTCGCTCTCGCGCTCCCTTCTGAAGGCTCTGGGCGGCTCTCGAGCGCGCGCGCTCGGCTTTGGCTC
 CACTCTCCGCGAGAACTTCACACTGTGGAGAGGCCAAAGAGTGCAGAGGCTCTGTTTGGAGATTTTCTTGGGAGA
 ATCTCGAGGCTCATTCATATTAGTGAAGTGTACCGCGCGGAGTGGCTCTAGAGTAACCAACAGTCTGTTCTGCGCTAGA
 GCRAATTCAGCGCATGTCGGTGGTCCCAATGCCATTTCTTTGGGAAAGATTTTGGAAAATAACATGGATGAGGATGG
 AGGTGGTGGTATGACCAAAACGAGGAGGAAAATGGGCCATCAGACAAATGATCATCGAGATGATTTTGGACCTTCA
 AATAAATATCAGAGTCAAGTGTCTTCAACAGCTCTAATATGGAGTATATGATCATGGGATGTAGAGCTGGAAAGT
 TCTCGAGATCTCTGGGCTGAAAGTTGCTGTGGGAACATGAGCCCTCGAGCTGCTTCCATCAATTTGACAGAGAT
 TTGGGAGGACACATCGGGGAGAGATATAGCGCCCGGACGCTTTCATGTACAATCTGTGTATGATGAAGTGAAGAAGCTT
 AGCTACCCATATGAACATGAATGCACACCCATTTGTCTCATTCAGGTGTTCTGGCGCTGTATGTATGACATATTACAC
 CAGCTCGTGTGGGACCATAGTAAACAGAAATCGGTTTGGCCAAATGAATTTGTCTATAAACATGAACATCTGGGGCGAG
 ATATGGGCGAAAGCTGTCTACTCTGTGTGCAATTTACTCCCAAGAGGAAATCTGTGGGGCGCTGCCCTTACAAA
 CTATGGGCGGCCCTGTTCTGCTTCCGACCTAGTTTGTGGAGGGGGCTGTAGAGAAATCTGTGCTCTCAAGAARAGGG
 TCAGACAGGTATATATCCCTCTCGAGAGAGGAAAACAAATAGGATAAGAACAGACAGATCAAGCTCAATGACATGACAC
 CATGTCCGGACCAAGTACAGATGATATAGTAGACAAATGAAGTCTATAGGCCACAGCAAAATGTCGCGCAATTTGTTCT
 TGTGAAGTAAAGATTAAGAGATCAGTCAAAAGGAAACAACTGCATATAGGTACAGATGTTCTGTGCTGGTGTGTGAT
 AGTAAAGCTAAAGTTTGTGGCAGTGATACATTATGAAGATGCATCCAGCATCTGTGATAGGCTCAATTCATTAATGT
 ATATAAGACATGATGATGGTGGTGGGTGATATCATAGACAGGAAGAAAGCATTTTCAATCAAGTCCAAATAGTAA
 AATGGTATTCAAAACAACTTGGCAAAATATGCTCAGTTCAATTCCTTCACAGTCTCTAAAGTAAAGATTTCTCAGGCTGT
 ACTTGTGAAAACAACTTGGGAAACGCTCTGTCAGTTCTCAATGCCCTGCTCTCATCTGCCAACAGATATGCTGTCT
 CTGTAACCTGTATGCAAGCAAAATCCAAATTTCTGCTGTGTAATTTGGAACCTCGATTTATCTGATCTGCTGCAATG
 TCGACAGACAGATACATGCTGGAGTGTTCTGAAATCCAGGTGGTATGTTGATGATATGCTGCTGGTGGACAAAGAC
 AAGACCTACATTCCTCTTTTCAGAAATGGAAATCTCTCAGAAAGATTCATACAGATCTCTCGAGGAGAAAGGCAATC
 AGAGTGTGTGCTGTGTGGTGAACATGAATCTTGGAAAGGACCATAAAGACATTTCCAATCGAATATTTCTGAT
 ATTTTCTGTATAAACTCTGATACATTTCTGTACAGAGTACATCAACTATTTTCAGCGCCAAAAGGTGGCCAAATGATAT
 TAAATCTGTGATAAACAAAGTCTATAAAATAAATACATGGGACATAGCTTTTGGGAAAGTAAATGAAATATCAATGG
 TTTTGAAGAACTCGTGTGTAATATTTGCTATATTTCTAGCAGTATTTTCTACGATTAATATACATGATCATGATT
 GTTCTACGTTTCAATATATATATGTTGCTTTGTATATGCGCTAACTAAATAAAGATCTAAACATTTGAATGTAAGT
 CGCCTCAGAAATCATCTAGTGCATTTTAAAAATATGCACTCTAAACCTAAAGAAACCTTATCACATTTTCTCCC
 AGTTCAATGCTATGACATATCAACCTCAAAATATCAAAATATTTCCATCTTAATATCTGAAAGTTTCTTTCT
 TGAATTTTAGGCTATAGAAATATTAATATTTGGAATTTGACTCTCTATTTTATATAAAATACCTTTTAAATATCT
 CAATAGATTCGTGTAATAATGTTTGTATCTCTTGGAAATGGCTTAAAAAATGAATGTAATAAAGTCTCAGAGTGGTGT
 ATGAAAACATCTCTGATGATCATGTAGTAAATGAGGGTTAAGACATGGACGACGAGAGCTTCTATGTATCTGTGTA
 AATTGAGTGACATCATTTTCTTTTGTGATCTGGCAATATCTCTCGACGAGAGATGATAATAGTCAAAAAGTT
 GACAAAGATGAACATGAATTTTACATATACCATTCGCACTGATTTTCTTTTAAAGTGTAAATGACCTTTGTATATA
 ATATATGTCATATCATGTGACCTTATAAGTGGATATATTTGTTCTATGAAAAGTATGTGCTGTTGTATACATAAA
 ATCTGTGAAATGTTAGTTTGTGTAAATTTTTTCTGCTGGTGGATTACATATTAATTTTTTCTGCTGGTGGGA
 TAAACATTAATATTAATCATGTTTCTAAAAAATTTTTTAAAAA

FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLLLEKYMDDEDGEWWIAKQRGKRAITDNDM
QSILDLHNKLRQSVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW
GRYRPPTFFHWQSWYDEVKDFSYPYEHECNPYCPFRCSGPFVCTHYTQVWATSNRIGCAINLC
HNMNIWGQIWPKAVYLVCNYSKGNWWGHAFYKHGRPCSACPPSFGGGCRENL CYKEGSDRY
YPPREEETNEIERQQSQVHDTHVTRSDSSRNEVISAAQQMSQIVSCEVRLRDQCKGTT CNR
YECPAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGI
QTIGKYQSANSFTVSKVTQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG
TRVYSIDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNP PGGKA FRV
FAVV

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

0978375.101601

FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG
CAGCGGAGCCAGCAGAGCCGGAAGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT
GGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCACGCCG
CGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGT
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC
AGCGACGTGAAGAAGCTGGAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT
CATCACCACCAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCAACCCCAAGCTGC
AGAGCACCAGCGCTTCATCAAGTGGTACAACGCTTGGAAACGAGAAGCGCAGGGTCTACGAA
GAATAGGGTGAAAAACCTCAGAAGGGGAAAACTCCAAACAGTTGGGAGACTTGTGCAAGGA
CTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTCT
TTTCTCAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTACCAACGGTCAG
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCAGATGGGAGACCCATCTCTTTGTGCT
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCTCTTTTAA
AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGA
GGAACAATGAGCTTGGTGGACACATTTCAATGCAGTGTTGCTCCATTCTTAGCTTGGGAAGC
TTCCGCTTAGAGGTCTTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT
GGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC
CTTAAAGAAGGTGTGGGGCTTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTGAGCAAAAACCTTAGGAGAAAACT
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA
AACCTTCAAAGCATGTTTCTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT
TTGTGATTCCCATGTAATCTTCAATGTTAAACAGTGCAGTCTCTTTTGAAGGCTAAGAT
GACCATGCGCCCTTCTCTGTACATATACCCTTAAGAACGCCCTCCACACACTGCCCCC
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTGAGAAACATTAGCAT
TGCATGCAAGTTTCATATTCTTCTAAGATGGAAAGTAATAAATATATTTGAAATGTAAAA
AAAAAAAAA

0976375.101601

FIGURE 149

MSLLPRRAPFVSMRLLAALLLLLLALYTARVDGSKCKSRKGPKIRYSDVKKLEMKPKYPH
CEEKMWIITTKSVSRVRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

Signal sequence:

amino acids 1-34

09978375-101601

DOWN THE

GCACCGACGACCTGCTATGCTTCTCTTGTTGTTTCACCCCGGTCCTGGCTATGTTAAACCTCCAACTGCTCTCTGTG
TATTAAGCTCTCTGCCATCAGTCTACCCCTCATCTGACGACCAAGCAGATCATCGTTGTACACAAATAATG
CAAAATTCGCGGGCCCTAAGAACACCGCTTACCACATGAGTCTTGGGTCAGTGGAGCATATATAGGGGTCCTCTA
TGCTCATCCCCCTCATGGAGAGAGGCGGTTTTCAGCGGCCCAAGCCCCGCTCTCTGAGTCGGCATTCGAAATCT
TACTCAGTTTGGCTGCTGTGTGCCCCAGCACCTGGATGAGAGATCTTACTGCTGATCATCTGCTCCATCTGTGT
TACCGCCAAATTTGGATATCTTTGGATGACCTATGTCAGAGTCAAAATGAGATCGCTCTTACTTAAACATCTAGT
GCCACGGAAGATGGAGGCCAACACAAGAAAGAACCGCAGATGATATAAACGATAGTACCGTGGTGGAGACGAAG
TATTCATGATCAGAACAGTAAAGAGCCCGTATAGTCTTATATCATCTGGGGATCTTACATGGAGGGCCACCGCAC
CATGATTGACGGGACAGTTTGGGACGATCCAGGAAGCCCATCTGATCACCATTAACTACCGTCTGGGAATCT
AGGTTTGTAAAGTACCGTGCACAGGACGCAAAAGCCCAATGTGGGCTCTGGATCAGATTCAAGCATCTCGGTG
GATTAGAGAGAGTTGGGAGCCTTTGGCGGGGAGCCCAAGAGATGACCATCTTCTGGCTCGGGGGCTGGGCGCTC
CTGTGTCAGCTGTTCACCTCTCCCATCTCAGAAAGTCTCTCCAGAGGCCATCTATTCAAGCGGGCACCGC
CTGTGTCAGCTGGGAGTGGAATCACACGCGCGGCAGTACTCTCGATATTGGCAGACAGTGGGCTCGGCTGCAATCT
GCTGGACACACCGCACGATGGTAAATGATGCTCGGGAACAGAACTCAAGGGGAGCTCATCCAGCAGCATCACTACCC
GGCCACCTTACCACATAGCTCTCGGGCGGGTGATGACGGCGAGCTCATCCGACAGCCCCAGACTCTGTAGTGA
CGAGGCGGAGTTCCTCAACTGCAGCATCATGCTCGGGCGTCAACCAAGGGGAAGGCCCTGAAGTTCTGTGACCGTAC
CTGGATGAACCGTCAAGTGTGACGGCCCAACGACTTTGACTTCTCGTCTCAACTCTGTGGACAGCTCTTACGG
CTACCTCTGAAGGGAAGACATCTTTGGGAGATCTCATAGTTTACTGACACAGATGGGCGCATGAAGGAACAAACC
GGAGCGGCGCGAAACCTCGTGGTCTCTTACTGACCACAGTGGGTGGCCGCCCGCGTGGCGCGGACCTCT
GCACGCGAGTACGGCTCCCCACCTACTCTTATGCTTTCTATCATCTGCAACGCGAAATGAAGCCGAGCTG
GGCAGATTCCGCCCATGTGTAGTGAGGTCCTTATGCTTCTTGGCATCCCATGATCCGCTGCTCCAGGAGTCTTCA
GTGAATCTTTTCAAGAGCTGCTCATGCTCAGGCGCGTGTGATCAACAAACCCAGGACCTTGAAGAGTGGGCTG
GTCCAAGTATAATCCAAAGACAGCTCTATCTGCTATTTGGCTTGAACCCAGAGTGAGAGATCATCTACCGGGC
AACGAAGATGGCTCTTCTGTGTGAATCTGTTCTCATTTGACATGTGAACAGAGATTTCAATGTGTTTCAAC
AACCAACAAGSTTCTTCCACAGCAGTACATCATTTCCCTATGGCACCGGCGATCTCCCGCAAGATATGGCC
AACCAACAAACCGCCAGCATATCTCTCTGCCACATCTCCCAAGCATCTAAGAGACCTCAACAAACAGGCGCTGA
AGCACCAACATGCTCTCATTTGAAGAACCAACGAGATTATTCACCGAATTAAAGTGCACCAATTGCCGTCCGGCGCTC
GCTCTCTTCTTCCATCACTTTAGCTTTTGGCGCGCTGTGATCAACAAAGGACAGAGGCGCCATGAGATCACAG
GGCGCCAGCTGCCCAGAGAAACACCAAAATGATATGCTGCATCATCAGAACAGAGAGATCATGTCTCTGCGAGT
GAGCAGCTGTGAACACGATACAGATGTGAGTGCCTGCAGGCACAGCAGCATCTAGGCTCACCCTGTCCGCGCAG
CTACACCTCTACGCTGCGCGGTGCGCAGATGACATCCATTAGAGCGCAACCAACCATCCATGATTTCCAA
CAGACTGACGGGGATCGACGCTTGGACATCTTTAAACCATCTCAGTGGAGGAACAAACGATCAAAATTTCCCA
CGCATCTTCCACATCAGATGATAGCTTTGCTCTTTTCCCTCTTATCCCTCTGCTCCCTACCGCTCAGCAACAT
AGNAGAGGGGAGGAAAGAGAGAGAGGAAAGAGAGAGAGAGAAAGATCTCCAGACAGGAATGTTTTTGTCCCAT
GACTTAAGACAAATAGTAAAGAGGAGCAGTACCTCCATCCGCGAGACCTTATGTTGTGTGTTTTCAGTATATAC
AAGATCAACTCTCTGACCTGTGAATATGTGAGAGTACACATTTCTGTAAATAATGCTCTTAAGATCTCTATPACA
CTCCATCAATGTTTGTGTGATAGGACATACCAATTTAAGGCCCGGGTGTTCACAGCTCATGAGAGAGCT
GACATCTGTGAACCTCAGCCAGGACAGTGAATTTTTTATTTATCAAGTGGAAAGTTAAACATTTCTTTCTGTG
CACACATATGATGCTCTCTCTTAAGCTGGAAGAAGTCAATGAGATTTTCCGAGCAGCATGGAGCTCTTATCTCAG
AGAGAGGAAAGCTGAGAAATTTATTATTAAGAAGATGGACTGTGCAGCGAAATCTGTACGGTTCTGTGCAAGAG
GTGTTTGTCCGAGCTGAACTATATTAAAGACCTTGT

FIGURE 151

MLNSNVLLWLTAIAKFTLIDSSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP
PTGERRFQPPPEPPSSWTGIRNNTQFAAVCPQHLDERSLLHDMPLTWFTANLDTLMTYVQDQN
EDCLYLNIIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGDPKR
VTIFGSGAGASCVSLLTLTSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVCNML
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLG
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIKFMYTDWADKENP
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEVFVY
FGIPMIGPTL FSCNFSKNDVMLS AVVMTYWTFNFAKTGDPNQPV PQDTKF IHTKPNRFEEVA
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPDMTS
FPYGTRRSPAKIWP TTKRPAITPANNPKH SKDPHKTGPEDTTVL IETKR DYSTELSVTI AVG
ASLLFLN ILAFAALY YKKDKRRHETHRRPSQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE
SLQAHDTLR LTCPPDYTLTLRRSPDDIPLMTPTNTITMIPNTLTGMQLHTFNTFSGGQNSTN
LPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

09078375.101501

FIGURE 152

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCTGTGGCAGCAGTGGCGGCGATGTTTGT
 CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTTGTGGGGTCTGGGCGAGGGGCCA
 CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAAACGGGAGCACTCGCTGTGGAAGCC
 CTACCAGGGTGTGGGCACAGGCAGTTCTCTACTGTGGAATCTGATGGGCAATGCCATGTGTGA
 TGACCCAGTATATCCGCTTACCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAAACCGG
 GTGCCATGTTTTCTGAGAGACTGGGAGTTGCAAGGTGCACCTTCAAATCCATGGACAAGGAAA
 GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC
 CTGTGTTTGGAAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT
 GAGGAGAAGCAGCAAGAGCGGGTATTCCCTACATCTCAGCCATGSGTGAACAACGGCTCCCT
 CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC
 GCAATCTTCATTACGACACCTTCTCGTGTGATTTCGCTACGTCAAGAGGCATTGACGATAATG
 ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCTGCC
 CCGCGGCTACTACTTCTGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA
 TTTCTTGAAGTTGTTTGAACCTGACAGTGGAGAGAACCCGAGAAGGAAAAGCTCCATCGA
 GATGTGTTCTTGCCCTCAGTGGACAAATGAAGCTGCCTGAGATGACAGCTCCATGCGCCG
 CCTGAGTGGCCCTGGCCCTCTCCTCATCGTCTTTTCTCCCTGGTGTTCCTGTATTTGCCA
 TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAGCGCTTCTACTGA
 GCCCTCCTGCTGCCACCACTTTTGTGACTGTCAACCATGAGGTATGGAAGGAGCAGGCACTG
 GCCTGAGCATGCAGCCTGGAGAGTGTTCCTGTCTCTAGCAGCTGGTGGGGACTATATTCTG
 TCACTGGAGTTTGAATGCAGGGACCCCGCATTCCTCATGGTGTGTCATGGGACATCTAACT
 CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC
 TTCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC
 AGAATTTATAGCCAGGCTGCCGTGTGTTTGACTCAGAAGGCCCTTCTACTTCAGTTTGT
 AATCCACAAAGAATTA AAAA CTGGTAACACCA CAGGCTTTCTGACCATCCATTCTGTGGGTT
 TTGCATTGACCCAACCTCTGCCTACCTGAGGAGCTTTCTTTGGAAC CAGGATGGA AACT
 TCTTCCCTGCCTTACCTTCCCTTCACTCCATTCACTGTCTCTCTGTGTGCAACCTGAGCTG
 GGAAGGCATTGGGATGCCCTCTCTGTGGGGCTGGGGCTGCAGAACA CACTGCGTTTCAC
 TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTTGGATCACTGTTCCCTAGCAT
 GGGTCTTGGGTCTATTGGCATGTCCATGGCTTCCCATCAAGTCTCTTCAGGCCCTCAGTG
 AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCTGGAAGACATCATGGATGCCATG
 GATTAGCTGTGCAACTGAC CAGCTCCAGGTTTGATCAAACCAAAGCAACATTTGTCATGTG
 GTCAGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTGTAGT
 TACGATTTTGGAAATCCCACTTTGAGTGCTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT
 GGGCTTGGATATGCCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAAGAGACAGT
 TGCTGTTCTCATGTTCCAAAGCTGAGAGCAACAGACCCCTCATCATCTGCTGCCCTGGAAGAGT
 CACTGTCATTGAGCAGCAGACGCTGAGTGCTGGCCTCTGTCAACCCCTTATTCCATGTCCTTA
 TTTTGAAGGGGTTCATGCTGCTCACCTTACTGCGCTGGGATTAATCAGTGTACAGGCCAG
 AGTCTCCTTGGAGGGCTGGAACCTCTGAGTCTCCTATGAACCTCTGTAGCCTAAATGAAAT
 TCTTAAATACCGATGGAACCAAAAAAAGGGCGGCCGCTCTAGAGTGC
 ACCTGCACTAGGATAACAGGGTAATAAGCTTGGCCGCATGG

09978375.101601

FIGURE 153

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911

><subunit 1 of 1, 348 aa, 1 stop

><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPLGSWQQWRRCLSDRGSRMLLLLLLLGSGQGQPGQVAGAGQTFEYLKREHSLSKPYQ
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGGALWNRVPCFLRDWELQVHFKIHGQKKK
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTPNEEKQQERVFPPYISAMVNNGLSY
DHERDGRPTLGGCTAIVRNLYHDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
YYFGTSSITGDLSDNHDVISLKLFEFTVERTPEEEKLHRDVFLLPSVDNMKLPENTAPLPPLS
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

Signal sequence:

amino acids 1-38

Transmembrane domain:

amino acids 310-329

0978375-101601

FIGURE 154

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGCCCTGGGACCATGGGCGTGAAGTGCATCTACGGATCAGTCT
 CTGATGGTGGGTGGTTAACTCAGTGGGACTTCAAGATTTCCATGAAGAAATCAGTGTCTTCTCATTCAAGAAAT
 TGGGTCTGGCTCAGAAATTCCTGCAGCTGGTGAAATCTGTCTTCTAGAAAGAGTTTAAATTAATGCTGCTGAGTCT
 GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAATAGAACTTAAATATGCTTTCCGCAACCGCTCT
 TGTGCTGCTGGCCCTGGCTGGCTGCTGGCTTTTGTAGAGCTCAGCTGCTGCTTCTCCACCTGATCCCGGTTCT
 CGACTCCTAAGAAATGGAATGAGTAGCAGAGTTCGAAAGAGAAATCATGCCCGACCTGTGACGGAGCCCGCTGTGA
 CAGACCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCAAGTGTGGCCGAGCGCAGCATGGAAGGTCAATGCC
 CGCATCATTTTAAAGCTGGTCTCAGTGTGATGTTCATTGCGCACGGAGCAGGTACCCCATGTATGTCTATTCCCA
 AAACAAAGCGCCAGAAATTTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAACTGGAAGCTTTCA
 TTAGTCACATCTCAAAAGGATCCGGAGCTCTTTGCAAAAGCCCTTGAATCTCTTGGCTCTTTACCCAAATCACC
 CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAAGCCGTGAGCTGCTGAGGGATA
 TCTATCTAAAGAAACACAACTCTGCCCCAATGATGTGTGTCAGACAGCTCTATTAGAGACCATGGGAAAA
 GCCGACCTTACAAAGTGGGCTGGCTTGTCTTTATGGCTTCTCCAGATTTTGACTGGAAGAGATTTATTTC
 GGCACACGCCAAGTGGCTGTCTGTCTGTGGAAGCTGCTATTGCCCGGTAAAGAACAGTATCTGGAAGAGGAGC
 AGCGTCTGTCAGTACCTCCTACGTTTGAAGAACAGCCAGCTGGAGAGAACCTACGGGGAGATGGCCAAAGTCTGG
 ATGTCGCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAAATGTGAGCT
 TTCCCTGTACCAAGAAATGGCTGTGTGTGACATGGAGCACTTCAAGTAAATTAAGACCCATCAGATCGAGGATGAAA
 GGGAAAGACGGGAGAGAAATTTGACTTCCGGTATTCTCTCTGGGTGCCACCCCATCTGAAACCAACCATCG
 GCCGATGTCAGCTGCCACCGAGGGCAGGAAAGAGAGCTCTTTGCCCTCTACTCTGCTCATGATGTCACTCTGT
 CACCGATTTCTCAGTGGCTTGGGCTTTTCAAGCCAGGTTCACAGGTTTGCAGCCAGGTGTGATCTTTGAGCTTT
 GGCAAGACAGAGAAAAGCCAGTGAACATTCGCTCCGGATCTTTTCAATGGCGTGCATGTCACTCCACACCT
 CTCTTCCGCAAGACCCACCAAGCGTCTCTCCAGCCCATGTGCCCGCTTGAAGTCTGGTCCGCTTTGTAAAA
 GGGACATGTTTGTAGCCCTGGCTGGTGTACAAATTAATGATGTCATGTCAAGGAGGATTCTAAAGG
 TAGCTAGTACAGCAGTATAGAAATCCATGCCAATACAGAGCATTAGGGAAGGTCCACTCTAGTTTGTCTGTTAC
 TAAGCTAGAAATATTGCTTTTAAAGCTTAAATATTGTTTGGGAACACAGAGTGTGGGGTTGAACAGT
 AAGCAGATTCGCTGAATGTGTGATGCTGCTGTTGTAACAAATGGCCAGTTACAGAGGAATAGAAGGTACTT
 TATCATAGCCAGACTCTGCTTAGAATGCCAGAAATATAGTGTGAAGAACAGCACACTCAACCAAAATTTTAAATCTTAGACAT
 TCTCTGGCTGGCCCATGTTACTATGTGATGGAACAGCACACTCAACCAAAATTTTAAATCTTAGACAT
 TTTACCTTGTCTTGTGAAGATTTCTTGAAGTGATTTATCTAAATAAAGTTGGCAACTTTTCTGAAGG
 GCCAGATTGAAATATTTCAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGCTCACTACTCACTCTCT
 TTTGAAAGCAGGAAAGCCACAGCAGTACATAAAGGAATTTGTAGCTGGTTCCAGGCCAGACAAACA
 GATGGTGACAGACTTGGCCCTGGGCTGTAGTTTGTGACCCCTCATCTAATAAATAGGCTATACACAAATG
 ACTTCCAGCATTGAGACGAGTTGAATACCAAGAATTATTCAATGGTTCTCCAGTAACCTCTGCTAGAAACA
 CAGAATTTGGTCTGTATCTGACATAGAACAAACCTTGAGGGTAAATAAATGAATTAGAATGAATCATAGAA
 AACTGATTAGAAGAACTTGTATGTTTATGATGATTGTGTACAGATAGTTTAAAGTATGTTCTAAATATTG
 CTGCTGTAGTCTATTGCTGTATATGCTGAAATTTTGTATGCCATTAGTATTTTATAGTTTAGGAAATATT
 TTTAAGACCGATTTAGATGACTTATTCTCTGTAGTAATATCAATTTGCTGTACCTGCTGTGGTGTAGAAG
 GAGCTAGAAGATGAATCAGGCATTTCTTCAATAAACTAATTATGGCTCATCCCTTTGACAAGCTGTAGA
 ACTGGATCATTTTAAACCAATTTTCACTAGTTTCAATGGTAAATTTCTGATTGATTTTAAATGGCTTTTGA
 AGAATTTGCTATTAGGTATTACAGATCTTTATAAGGTGTTTATATATTAGAGCAATTATAATTACATCTG
 TGATTTCTGAACATAAGGTGCTAATTAGAGAAATGGAAGTGAAGTGAAGTCTCTGTTGTATCGGCATTC
 AACTTTTCTGTTGTTTGTCTCAGTGTGTGCAATTTGAATATGCTGTTCTATAAATAAATTTTAAAGATAA

FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLALLAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDPVTEPPVTDPVY
EALLYCNIPPSVAERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMCHFCNVSFPC
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQITGRMQRATEGKEELF
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSSEHSVRILYNGVDVTFHTSF
CQDHHKRSKPKMCPLENLVRVFKRDMFVALGGSGTNYDACHREGF

Signal sequence:

amino acids 1-18

00070375-104641

FIGURE 157

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILGLTLWETGCTQIRYSVPPEELEKGSRVGDISRDLGLEPRELAER
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDIILMEDKVKIYGVVEVEVR
DINDNAPYFRESELEIKISENAATEMRFFPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA
DGSKYPELVKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFYVDDKAAQVFKLDCNSGTISTIGELDHE
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLVN
DQDSEENGQVICFIQGNLPFKLEKSYGNYSLVTDIVLDREQVPSYINITVTATDRGTPPLST
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLSVSTAHDPCENNAQITYSLAENTI
QGASLSSYVSINSDTGVLYALSSFDYEQFRDLQVKVMARDNGHPPLSSNVLSLFLVDQNDN
APEILYPALPTDGS TGVELAPRSAEPGYLVTKVAVDRD SGQNAWLSYRLLKASEPGLF SVG
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSI PQVLADLGSLES PA
NSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLLQASGGGLTGAPASHFVGVD
GVQAF LQTYSHVSLTTDSRKSHLIFPQPNYADMLVQS ESFEKSEPLLSGDSVFSKDSHGL
IEVSLYQIFFLFFFNCSVSQAGVQRYDHSSLRPQT PRLKQLSHLCLRCNRDYRCKPPTVCLS
IYLSIYLSIYLSIYLLLSCTDGS LTPVIPVLWEAEAGGSPEVGS LRPA

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

0978375-701664

FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA
TCAGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCAATGGGACGCCCCCGACCTCGT
GCGGCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC
ACAGGAGGACAAGGTGCTGGGGGGTCAAGAGTGCCAAACCCCAATTCGAGCCTTGGCAGGCGG
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCTT
ACAGCTGCCCCTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA
TAAAGATGGCCAGAGCAAGAAATACCTGTGGTTTCACTCCATCCCACACCCCTGCTACAACA
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATGCACCCAGCCTGGCCAGAAGTG
CACCGTCTCAGGCTGGGGCACTGTCAACAGTCCCGAGAGAAATTTTCTGACACTCTCAACT
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCGGGGCAGATCACA
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG
CCCCCTGGTGTGTGATGGTGCACCTCCAGGGCATCACATCTGGGGCTCAGACCCCTGTGGGA
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCT
CTGGTTC

0978375.701601

FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGGQQLLCGGVL
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPQEIPVVQSIPHPCYNSSDVEDHNHDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGDGGGLVCDGALQGITSWGSDDPCGRSDKPGVYTNICRY
LDWIKKIIGSKG

Important Features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

09078375-101601

FIGURE 160

GGCGCCGGTGACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCG
CGCGCCCCACGCCCAACCCCGGCCCGCGCCCTAGCCCCCGCCCGGCCCGCGCCCCG
GCCCCGCCCCAGGTGAGCGCTCCGCCCGCGCGAGGCCCGCCCGCCCGCCCCCGCCCCG
CCCCGGCGCGGGGGAACGGGCGGATTCTCGCGCTCAAACCACTGATCCCATAAAA
ATTATCTCTCCCGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCGCGCGCCCTCG
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCAGCCAGAGCCGGGCGGAGC
GGAGCGCGCGAGCCTCTGCCCGCGCGGGGCCGGGCGCGGCTAGCGCGCGCGCCTTGA
TGCGGACCCCGCGCGGGGAGACGGCGCCCGCCCCGAAACGACTTTCAGTCCCCGACGCGC
CCCGCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGCTGCTGGCATGGGTG
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA
GCCCAAGGTGACGACAAGCTGCCCGCAGCAGGGCTGCAGGCTGTGCCCGTGGGCATCCCTG
CTGCCAGCCAGCGCATCTTCTGCAAGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC
CGTGCTGCCGCAACCTCACCATCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGC
GGCTGCCCTTCACTGGCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCAAGCTCC
GGTCTGTGGACCTGCCACATTCACAGGCCCTGGGCCGCTACACAGCTGCACTGGACCGC
TGCGGCTTGCAAGAGCTGGGCCCGGGGCTGTTCCGCGGCTGGCTGCCCTGCAGTACCTTA
CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA
CACACCTCTTCTGCAAGGCAACCGCATCTCCAGCGTGGCGAGCGCGCTTCCGTGGGCTG
CACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGATGCCTT
CCGTGACCTTGGCCGCTCATGACACTTATCTGTTTGGCAACAATCTATCAGCGCTGCCCA
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCACTAGGCTCAACGCAACCCCTGGGTG
TGTGACTGCCGGGACGCCCCACTCTGGGCTGGCTGCAGAAAGTTCCGCGCTCCTCCTCCGA
GGTGCCCTGCAGCCTCCCGCAACGCGCTGGCTGGCCGTGACCTCAAACGCGCTAGCTGCCAATG
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGCAGGGCCACC
GATGAGGAGCCGCTGGGGCTTCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCTCAGT
ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTG
ACAGCCCCCGGGCAACGGCTCTGGCCACGGCACATCAATGACTCACCTTTGGGACTCTG
CCTGGCTCTGTGAGCCCCGCTCACTGCAGTGCAGGCCGAGGGCTCCGAGCCACAGGGTT
CCCCACCTCGGGCCCTCGCCGAGGCGAGGCTGTTTCAACGCAAGAACCGCACCCGAGCCACT
GCCGTCTGGGCGAGGCAGGCAGCGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC
CTACCCAGCCTCACTGCAGCCTCACCCCCCTGGGCTGGCGCTGGTGCTGTGGACAGTGCT
TGGGCCCTGCTGACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC
GGGTCTCTCTCCACGCCGCCAAGCCAGCCGGGCGGCCGACCGTGGGGCAGGCCAGGCCAG
GTCTCCTCTGATGGACGCTTGCGCCCGGCCACCCCATCTCCACCCCATCATGTTTACAGGG
TTCCGGCGCAGCGTTTGTTCAGAACGCCGCTCCACCCAGATCGCGGTATATAGAGATAT
GCATTTTATTTTACTTGTGTAAAAATATCGACGACGTGAATAAAGAGCTCTTTTCTTAAA
AAAA

0978375.101601

FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184

><subunit 1 of 1, 473 aa, 1 stop

><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRLLAWLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAAASQRI
FLHGNRIISHVPAASFRACRNLTILWLHSNVLARIDAAAFGLALLEQLDLSDNAQLRSVDPA
TFHGLRLHTLHLDRCLQELGPGLEFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLLHQNRVAHVHPHAFRDLGRIMTLTYLFANNLSALPTEALAP
LRALQYLRNLNDNPWVCDRCRARPLWAWLQKFRGSSSEVPKSLPQRLAGRDLKRLAANDLQGCA
VATGPYHPIWTGRATDEEPLGLPKCCQPDAAKASVLEFGRPASAGNALKGRVPPGDSPPGN
GSGPRHINDSPFGLTPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA
GSGGGGTGDSESGALPSLTCSLTPLGLALVLWTVLGP

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

0078375-101604

FIGURE 162

GGAAGTCCACGGGGAGSCTTGGATGCCAAAGGAGGACGGCTGGGTCTCTGGAGAGGACTAC
 TCACTGGCATATTTCTGAGGTATCTGTAGAATAACACAGCCTCAGATACTGGGGACCTTAC
 AGTCCACAGAACCGTCTCTCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCACGGGGA
 AGCTCATTTGCAGACAAAGGCAAGTCTCTTTTCTCTCTTTTGGGCTTATCTCTGGCG
 GCGCGCGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGTCTCTTTGTGCAC
 CAATTTAGCAAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGGTAGGGTTG
 TTTCCAGAGGGAAACAACTACATTTCAGCTCAATCAGGAGACCGCGGATTTGTGTCTAAAT
 GAGAAATTGGACCGTGAGCAATCTGTGCGGTCAACAGAGCCCTGTGTGCTAGCTTTCCAAGT
 GTTGCTAGAGAGTCCCTTCGAGTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC
 ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCTCTCTGGG
 ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA
 TATAATCAGCCCCAACTCTTATTTTCGGGTCTCACCCGCAACCGCAGTGATGGCAGGAAAT
 ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAAAC
 CTCACAGCATGGATGGTGGCTCTCCGCCAGATCTGGCACTGCTCAGGTTCTACATCGAAGT
 CCTGGATGTCAACGATAATGCCCTGAATTTGAGCAGCCTTTCTATAGATGTCAGATCTCTG
 AGGACACTCCGGTAGGCTCTCTGGTTGTGAAGTCTCTGCCCGGATGTAGACACAGGAGTCA
 AACGGAGAGATTTCTTATTTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAAACCTTTAAGAT
 CAATCCCTTTGACAGGAGAAATGAACTAAAAAAACAACTCGATTTGAAAAAATCTCAGTCTT
 ATGAAGTCAATATTGAGGCAAGAGATCTGGAAACCTTTCTGGAAAAATGCACCGTTCTGATT
 CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT
 ACCTGAGAACCGCGCTGAAACTGTGGTTGCACTTTTCAGTGTCTCAGATCTTGATTCAAGAG
 AAAATGGGAAAAATTAGTTGCTCCATTGAGGAGGATCTACCCCTTCTCTCTGAAATCCGCGGAA
 AACCTTTACCCCTACTAACGGAGAGACCCTAGACAGAGAAAGCAGAGCGGAATACAACAT
 CACTTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC
 TGATCGCGGATGTCAATGACAAACGCTCCCGCTTCACCCAAACTCTACACCTGTTCGTCTC
 CGCGAGAACCAACAGCCCCGCGCTGCACATCCGACGCGTCAGCGCTACAGACAGAGACTCAGG
 CACCAACGCCAGGTCACTACTCGCTGTGCGGCCAGGACCCGCACTGCCCTGCCCTCACAT
 CCTGGTCTCTCATCAACCGCGGACACCGGCACCTGTTGCGCCTCAGGTTCTTGGACTACGAG
 GCGCTGCAGGGGTTCCAGTTCCGCGTGGGCGCTTCAGACCAAGCTCCCGCGCTGAGCAG
 CGAGGCGCTGGTGCGGTGGTGGTGCTGGACGCCAACGACAACTCGCCCTTCGTGCTGTACC
 CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCGGGCGCGGAGCCGGGCTAC
 CTGGTGACCAAGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACCGCTGGCTGTGTAACCA
 GCTGCTCAAGGCCACGGAGCTCGTCTGTCTGCGCGTGTGGGCGCACAAATGGCGAGGTGCGCA
 CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGTGTTGCAAGGAC
 AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCTGGTGGACGCGCTCTC
 CCAGCCCTACCTGCTCTCTCCGAGGGCGGCCCGACCCAGGCGCAGGCGGACTGTCTCACCG
 TCTACCTGGTGGTGGCGTCTGGTGTCTCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 GTGGCGGTGCGGTGTGTAGGAGGAGCAGGCGCGCTCGTGGTGGTGGTGGTGGTGGTGGTGGT
 GGGCCCCCTTCAGGGCATCTTGTGGACATGAGCGGCACAGGACCCCTATCCAGAGCTACC
 AGTATGAGGTGTGTCTGCGCAGGAGCTCAGGACCAATGAGTTCAAGTTCCTGAAGCCGATT
 ATCCCCAACTTCCCTCCCAGTGCCTGGGAAAGAAATCAAGGAAATTCTACCTTCCCCCAA
 TAACTTTGGGTTCAATATTCAGTGACCATAGTTGACTTTTACATTCATAGGATTTTATTT
 TGTGGCAATTCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGAATATTGTACGGAT
 TTACTCTTGATTTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT
 CCTGGTTCTT

0978375-101601

FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLI CRQRQVLFSLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR
RGVRVVS RGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLR FQVLLES PFEFFQAE LQV
IDINDHSPVFLDKQMLVKVSESSPPGTT FPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR
SDGRKYP ELVLDKALDREEEAELRLTLTALDGGSPPRS GTAQVYIEVL DVNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATD VDTGVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
DLDSGENGKISCSIQEDLPFL LKSAENFYTL LTERPLDRESRAEYNITITVIDLGTPLMLITQ
LNM TVLIADVNDNAPAF TQTSYTLFVRENNSPALHRSVSATDRDSGTNAQV TYSLLPPQDP
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELG LFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAQ
ADLLTVLYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGLPLGHLVDMMSGTRT
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFP PQCPCKEIQGNSTFPNNFGFNIQ

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

09/03/25, 10:00

FIGURE 164

ACCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCGGTAGCCGTGC
GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCGCGTCAT
GCGGCTCCTCGGCTGGTGGAAGTATTGCTGTGGGTGCTGGGACTTCCCCTCCGCGGCGTGG
AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG
TGATTCTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGCGGGAATCTGACG
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG
GAGAGAAACATTACAGGAATTAGAAAATTTCACTCTGAAAATTTTAAATATGTACAGGACCT
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCTCTGTTTTACACCCCGTGGT
GCCGCTTTTCTGCCAGTTTGGCCCTCACTTTAACTCTCTGCCCGGCATTTCAGCTCTT
CACTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC
TGTTCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC
GAACACTGGAAACACTGAAAATCTTCATTTTTAATCAGACAGGTATAGAAGCCAAGAAGAT
GTGGTGTTAACTCAAGCCGACCAAATAGGCCCTCTTCCAGCACTTTGATAAAAAGTGTGGA
CTGTTGCTGTGATTTTCTTATTCTTTTAATTAGTTTTATTATGTATGCTACCATTCGAA
CTGAGAGTATTCGGTGGCTAATTCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT
GAAAGAAGTTGGAAGAGGAACTTCAATCCTTCGTTTCAGAAATAGTGCTACAGTTTCATA
CATTTTCTCCAGTGACGTGTTGACTTGAAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC
AAAAATATTCAATAG

0978375.101604

FIGURE 165

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333

><subunit 1 of 1, 360 aa, 1 stop

><MW: 39885, pI: 4.79, NX(S/T): 7

MVPAAGRRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEBQPAHPLQVGAVYLGE
ELLHDPMGQDRAAEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTGAGGAEDSRC
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE
NFTLKILNMSQDLMDFLNPNNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS
QHSSLSTRFGTVAVPNILLFQGAKPMAFNFHTDRTLETCLKIFIFNQGTGIEAKKNVVVTQADQ
IGLPLSTLIKSVDWLLVFSFLFLISFIMYATIRTESIRWLPQGQEHVE

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 321-340

Homologous region to dilsufide isomerase

amino acids 212-302

N-glycosylation site.

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281
and 293-296

Thioredoxin domain

amino acids 211-227

00978375-701604

FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTGCGCGGCCACGATGCTGCAGGGCCCTGGCT
CGCTGCTGCTGCTCTTCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGGGGCTCTTCTCTC
TTTGGCCAGCCCGACTTCTCTTACAAGCGCAGCAATTGCAAGCCCATCCGGTCAACCTGCA
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGACCA
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCCTGGTTCATGAAGCAGTGCCACCCG
GACACCAAGAAGTTCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC
CATCCAGCCATGCCACTCGCTCTGCGTGTCAGGTGAAGGACCGTGGCCCCGGTTCATGTCCG
CCTTCGGCTTCCCCTGCCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAACGCTTTGTAAAAATG
ATTTTGCACGTAAAAATAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGACCTGTGAGGAGATGAACGACATCAACG
CGCCCTATCTGGTTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG
TGGCAGAAGGGGAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA
GTCCCGGCATCCTGATGGCTCCGACAGGCCCTGCTCCAGAGCACGGGTGACCATTTCTGCTCC
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCTGTAGTTATAAGGCCACAGGAGTG
GATAGCTGTTTTACCTAAAGGAAAAGCCACCCGAATCTTGTAAGAAATATTCAAACATAA
AAATCATGAATATTTTAA

09/03/95, 10:50:1

FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920
><subunit 1 of 1, 295 aa, 1 stop
><MW: 33518, pI: 7.74, NX(S/T): 0
MLQGPGSLLLLLFLASHCLGSARGLFLFGQPDFS YKRSNCKPIPVNLQLCHGIEYQNMLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDDETIQPCHS LCVQVKDR
CAPVMSAFGFPWPDMLECDRFPQDN DL CI PLASSDHLLPATEEAPKVCEACKNKND DDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSE RDLKKS VLVWLKDSLQCTCE
EMNDINAPYLVMGQKQG GELVITSVKRWQKQREFKRISRSIRKLQC

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

00978375.104001

FIGURE 168

GTGGAGGCCGCCGACATGCGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTGTCTCGCGATC
AGCCTGTCTCACTGTCTCAAACGCCACGTGTGGCTCAGCTTTGCACCTGTGGCTGACGTGTCAT
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGCG
ACCATCTGGGTGCGTGGCTGAACCTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGTCATGGT
TGTGGGACCCAAAACCCATTTGCCCTTCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCCAGAGCACCGACGA
GCCACGGCCAACATGCTCGCCACCATGTGCAACCTCTGGGCGTCTTGTGGCCAATGTGCT
GTCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCGGTTAATGTCGCGTGTCTATACCATCC
CTGCTGGCGTCGTCTGCCCTGTGTCCACCATCTGCCCTGTGGGAGAGTGTGCCCCCACCCG
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCTGGATGGGCTCAAGCTGCAGCT
CATGTGGAACAAGGCCTATGTATCTTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTTC
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTTA
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG
CCTGCGTGCCCTTTGCCCTGGTGTCCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC
TGCTCGCTGTCTGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTGCA
GTGTTCTTCTCCCGTGGGGGAGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCAGCGCTCGGAGCCGTCTCTG
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGTGATGGCCGG
CCTGTGCACCTTCTTACAGTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG
GGTGTGGACCGAGGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCACGACGGCGACTCCGGA
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGGAGCCCCACCCAGCCT
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCCCCCCCGGC
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCTCTT
CTCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGGCGGCT
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

FIGURE 169

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988
><subunit 1 of 1, 560 aa, 1 stop
><MW: 58427, pI: 6.86, NX(S/T): 2
MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTON
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSFVLV
KKGEDIPMLGVYTTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK
HFTEATKIGLCLFSLACVPFALVSQLOQQTALALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEGAATGMIFVLGQAEGLIMLAMTALTVRREPSLSTCQQGEDPLDWTVSLLL MAGLCTFF
SCILAVFFHTPYRRLQAESGEPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSPWPVIT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,
280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

FIGURE 170

GTCCACATCTCTGCTCAACTGGGTCAGGTCCCTCTTAGACCAGCTCTTGTCATTGTGCTGAAGTGGACCAAC
 TAGTTCCCAAGTAGGGGGTCTCCCTTGGCAATTCTTGATCGGCGTTTGGACATCTTCAGATCGCTTCCAATGAAGA
 TGGCCTTGCCCTGGGGTCTGCTGTGTTTCAATAATCATCTAACTATGGGACAGGTTGTGCGCGGAGCTCTGGGGG
 AAGGAGCACGGGGCTGATCAAGCCATCCAGGAACAATCGAGGACTTGTCCAGGCTTGAAGAAGACTCTAGTGTT
 TCTGAATCTAGCCCACTTGGCGGTAAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCGAGGTGC
 CTACTTATTTCTTTAGGGGATGTCAGAGGTGACCATCTCACGGTGAATACCAAGTCTGCAGAGGAAGTGCC
 ATCTGGTACAGTGTATCGGGAAGACTGTCCCAGGAATCTGGGCGGAGGAGAGCGGAGGCGCAAGCTGGGCGCGCTCT
 CCAGGTGTTGCAAGCTGCTCAGGCGCTCCCAATTCAGGTGGAATCTTGAGGAAGGCTTGTCTAGCACAGCAAGCG
 CTGTGATCGAGAGCAGCTGTGCGGACAGTGGGATCCCTGCTGTTTCTTTGATGTGCTTGCCAACAGGGAATTT
 GGCCTCTGATCCATGTGGAGATCCAAGTGTCTGGACATCAATGACCACAGCCAGCGTTTCCCAAGGCGGAGCAGGA
 CTGTGAATCTCTGAGAGCGCTCTCTGCGAACCAGGATCCCTGGAGCAGAGCTCTTGACCCAGACACAGGCCC
 TAACACCCCTGCACACTCACTCTGTCTCCAGTGGAGCACTTGGCTTGGATGTCTATGTGGGCGCTGTAGTACAG
 CAACATGCAAGACTCATAGTGGTGAAGGAGCTGGACAGGGAATTCATTTCATTTTGTATCTGTGTAACTGTC
 CTATGACATGGGAACCCCCCAAGTCAGGTACCAAGCTTGGTCAAGGTCAACGCTCTTGAAGTCCCAATGACAAATG
 CCTCGCTTGTCTGAGAGTTCTACTGGCATGGAAATCCAAGAAGATGCTGCACCTGGTACGCTCTCATAAACT
 GATGCCACACAGCCCTGACCAAGGCCCCAATGGGAGGTGGAGTTCTTCTCAGTAAGACATGCTCCTCAGAGGT
 GCTGGACACTCTCAGTATGTATGCGCAAGACAGGCGAGGTCACTTCTGCTCGACTCTTAGACTATGAAAAGAACCC
 TGCTTACGAGGTGGATGTTTCAGGCAAGGGGACTGGGTCCAATCTATCCAGGCCATTGCAAGTCTCTCATCAA
 GGTCTTGATGTCTCAATGACAACTCCAAAGCATCCAGTCACATGGGCTCCAGCCATCACTGTGTTCAGAAGC
 TCTTCCCAAGGACAGCTTTTATGTCTTGTCTATGGCAGATGACTTGGATTTCAGGACACAAATGTTTGTGCTCAATG
 CTGGCTCTGGAGCAGAGCTGGGCACTTCAGGCTGAAAAGAACTAATGGCAACACATACATGTTGCTAACCAATGC
 CACACTGGACAGAGAGCAGTGGCCCAAGATATACCTCACTCTGTAGGCCAAGACCAAGGACTCAGGCCCTTATC
 AGCCAAAGAACAGCTCAGCTCAGTCTCAGTTCAGTGCATCAACGACATGCACTGTGTTTGAAGAAAGTCTATGA
 AGTCTCAACCGGGAAACCACTTACCTCTCTTCACTCATTACATCAAGGCTCATGATGCAGACTTGGGCAAT
 TAATGGAAAGCTCTATACCCGATCAGGACTTCCAGTGTCTCACTAGTAGTACTTGTAGCTCAACACAGAGAGA
 GGTCACTCTCAGAGTCTGATGAATCTGAAGAGATGGCGGCTTGTAGTTCCAGGTGATGCGACAGGAGAGCGG
 GCACCCATGCTTGTCATCCAGTGTCTCTGTGTGGGTCAAGCTCTTGGATGCCAATGTAATGCCCCAGGAGGTGGT
 CCAGCTCTGTCTCAGGATGAAAAGCCAGCCTCTCCGTGCTTGTGATGCTCCACAGGCACTCTGCTGTGTGCC
 CTCTGAGACTCCCAATGCTTGGCGCTGGCGGCACTGACACACTCACTGGCCATCTCAGCTCCCGCCATG
 CTTTGTGACAACTTGTGGCAAGATGCAAGTCTGGGCGCAATGGAGAGCCCTCTACAGCATTCGCAATGG
 AAATGAAGCCCACTCTCATCTCTCAACCTCATACGGGCGAGCTGTTCGTCAATGTCAACATGCGCAGCGCT
 CATTGGGAGTGTGGGAGTGGAGATAGTACTAGAGGACCGAGGAAGCCCCCTTACAGACCAGGCCCTGTT
 GAGGTCATGTTTGTCCAGGTGTGGACCACTGAGGACTCAGCCGCAAGCTCTGGGCGTGTGAGCATGTGAT
 GCTGACGCTGATCTGCTGGCTGTACTGTTGGGATCTCTCGGCTGTGCTTGTCTTGTTCATGTCTATCTGGCG
 GACAGAAAAGGAAGACACAGGGGCTTCAACTGTGCGGAGGCGGAGTCCACTACCGCAGCAGCCCAAGAGGCC
 CCAGAAACACATTCAGAAGGCGAGACATCCAACCTGCTGCTGTCTCAGGGGTGAGGCTGTGAGCTGTGAGT
 CGGGCAGTCCACAAAGATGTGAGCAAGGAGGCGATGATGGAAGCAGGCTGGGAGCCCTCGCTGAGGCCCTCT
 CCACCTACCCCGACCTTGTAGCAGGACGCTGCTAATCAAGCAACAGGAGACCCGCGGAGGCGGAGAGT
 GCTGCAAGACACGGTCAACCTCTTTCAACATCCAGGACAGGAGATGCTTCCCGGAGGACCTGTGAACCTTCC
 CGAGCCCGAGCTTGCACAGGCGAGCCAGCTTCCAGGCTCTGAAGGTGTCAGGACAGCCCAAGGAGGCTGAC
 TGGAGACAGGGCAGTGAAGAAAGCCACAGAGGCCACAGGCTCTCTTGCACACCTGAGACGGCAGCGACATCT
 CAATGGCAAGGTGTCCCTTGAGAAAGAACTCAGGGCCCCGTAGATCTGTGCGAGGCTGTGCTGTGCTGTGCT
 TGCTTCTGCGGAGCGGACACCCGCTGGAGGAGCTCACTGTGGAATCTCTCTCTGTTGACAAATCTCCAGCTGTCT
 GTCTTGTGTCATCAGGGCCAAATTCAGCCCAACCAACACCGAGGAATAAGTACTTGGCAAGACAGGAGG
 CAGCAGGATGCAATCCAGACACAGATGCCCAGTGAAGGCGTGGAGGACGACAGACCCAGAAACAGGAGGA
 AGGGCTTTTGTGCTCTGAAGAGGACCTCTCTGTGAAGCAACTGTGAGAAGAGCTGTCAAGTCTGTGTGACCC
 CAGCACAGGTCTGGCCCTGGACCGGCTGAGCGCCCTGACCCGGCTTGGATGGCGAGACTCTTTTGGCCCTTAC
 CACCAACTACGTGACAAATGTGATCTCTCCCGGATGTGTCAGCAACGAGGAGCGGAGGACCTTCCAGAGTTCGG
 CAAGGCGAGGCGACAGGTGAGGCCCAACAGGCAAGGCTGGCCAGCACTTGTCTCGAGATGAGCTCACT
 GCTGAGATGCTGCTGGAACAGCGCTCAGCATGCCGTGGAGGCGCTCTCGAGGCGCTGCGGAGGCTCTCGGT
 CTGCGGAGGACCTTCAAGTTAGACTTGGCCACAGTGCAGCTCAGGCAATGAAGTCAAGGAGGACCCAGGTG
 AAGACCGGGACTGAGGCGAGTGAAGACAGGACAGCAGCAGCAGCAGGTGCTGTGAACATCACTCAGAGCGCT
 CTGATCTCAAGAACCGGGGCTGAGATCTGTGACAGAGAGTGGTTTCAAAATCTGTGAATCACTCAGTGTAG
 CGCGGCTGTGAACACTTTAGGTGTACTGTGCTACCCCAACAGGAGGACAGGCGCCAGGACTCAACAGCTGAC
 TGACCAAGCAGCCCTTGAAGCAGCTCTGAGTCTTTGGAGACAGGAGCGGTTGTGGCTGAGATGAAGTGT
 TCCCTGAACAAATATGTGGAGCAAAAGGCTCAGTCTTGGCAACAGATGTCAGCAGGATCAACAGGATG
 AAAGGCTGGCTCTTGGGTAGCAGGAGTCAGGCGGCTGTACCTGGGCGTGCAGGAATGCTCTGACCTAT
 CARTAAGGAAAAGCAGTAAAAAAGGAAAAA

FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331
<subunit 1 of 1, 1184 aa, 1 stop
<MW: 129022, pI: 5.20, NX(S/T): 5
MMQLLQLLLGLLPGGGYLFLLGDCQEVTTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSVFDVLATGDLALIHVEIQ
VLDINDHQPRFPKGEQELEISSESASLRTRIPDLRALDPDTGPNTLHTYITLSPSEHFALDVIV
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNSPFAFAESS
LALIEQEDAAPGTLTIKLATDPDQGPNGEVEFFLSKHMPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGPNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLTLLAQD
QGLQPLSAKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVS
YRIQDSPVAHLVAIDSNTEVTQAQRSLNIEEMAGFEFQVIAEDSGQPMCLASSVSVVWSLLDA
NDNAPEVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPPLATHSSRPFLTT
IVARADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMMLTVICLAVLLGIFGLILALFMSICRTEK
KDNRAYNCREAESTYRQPKRPQKHIOKADIHLVPVLRGQAGEPCEVQGSHKDVCKEAMMEA
GWDPCLOAPFHLTPPLYRTLNRNQGNQGAESREVLQDTVNLLFNHPRQRNASRENLNLFEP
QPATGQPRSRPLKVAGSPTGRLAGDQGSSEAPQRPASSATLRRQRHLNGKVSPEKESGFRQ
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGGFQPKPNHRGNKYLAKPGGS
RSAIPDTDGPSARAGQTDPEQEEGPLDPEEDLSVKQLLEELSSLLDPSTGLALDRLSAPD
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTTFQTFGKAEAPLSPTGTRLASTFVSEMSSL
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSLDLATSAAAGMKVQGDGPGGKTGTGEGKSRGSS
SSSRCL

Important features:

Signal peptide:

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

09978375.101601

FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGG
 CAGACCGTGTGAGGGGGCCGTGTGGCCCGAGCGTGTGTGGCCTCGGGGAGTGGGAAGTGGAG
 GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT
 CCCAGATACTATTTTTTGGATTGGGTGGCTTTTCTTATGCGCCAATTGTTAAAGACTAT
 GAGATACGTCACTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCAATTTCTTGCACCAT
 GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT
 GGAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTACATTGGC
 TATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAAGACTGCTTTTTTCTGTCTCTT
 ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTCCCATTTCTCAGCCCAA
 AACATGGGATCTTATCATAGAACAGCTCATCAGCCGGTTGGTGTGATTGGAGTGACTCTC
 ATGGCTCTCTTTCTGGATTGGTGTCTCACTGCCATACACTTACATGTCTTACTTCCT
 CAGGAATGTGACTGACACGGATATCTAGCCCTGGAACGGCGCATGCTGCAAAACCATGGATA
 TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA
 GTGCATAACAAACCATCAGGTTTTCTGGGGAATGATAAAAAGTGTACCACCTCAGCATCAGG
 AAGTGAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC
 TTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC
 AAGGGGAAATATTTAATTTTCTGGTTACTTTTCTCTATTTACTGTGTTTGGAAAATTTT
 CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAACGGATCCTGTGACAAAGAGGCA
 TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT
 TCCTTCATCTTGTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC
 CAAGTTCTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCTGCTATTAGCAC
 AGATAATGGGATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCCTTAGAA
 TACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCCTTGGTT
 TGATGTGATCTTCTGGTCAAGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAAC
 AGGCACCAGAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT
 GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAAGGCCCTGACATTTTATAAAC
 AAACAAAATGCTATGGTAGCATTTTTCACCTTCATAGCATACTCCTTCCCGTCAAGTGATA
 CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA
 GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAAGAACTAA
 AGGTGAAAAATACACTGAACTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT
 AGGATTTCCGTTTTAAGGTTACATGGAAGGTTATAGCTTTGCCCTTGAGATTGACTCAIT
 AAAATCAGAGACTGTAACAAAAAAGGCGGCCGCGACTCTAGAGTCG
 ACCTGCAGAAGCTTGGCCGCATGCCCCAAGTGTATTGACGCTTATAATG

00070375.101601

FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAPFSCTMFELIIFEI
LGVLNSSSRYPHWKMNLCVILLILVFMVPPYIGYFIVSNIRLLHKQRLLFSCLLWLTFFMYFF
WKLGDPPFPIILSPKHGILSIEQLISRVGIVGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTCKFFYAIS
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

09078375-101601

00000000

CATGGGAAGTGGAGCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGATCCAGCA
TCATGATTACCTCCNGANACTATTTTTGGGATTGGGTGGCTTTTCTCMGCGCAAATGTT
TAAAGACTATGAGATACGTACGATATGTTGTACNNGGTGATCTTCTCCGTGACGTTTGCCATT
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT
TATTTTCACTGAAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTNCATGGTGCCTTT
TTACATTGGCTATTTATTGTGACGAAATCCGACTACTGCATAAACACGACTGCTTTTTT
CCTGTCCTTATGGCTGACCTTTATGATATTTCCAG

FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCCGGGTTNNGNATACCTTCCCAGAAAAATATTTTTTGGATTTGGGGTAGNTT
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCCTTATTTTCACTGGAAAAATGAACCTGTGTGTAATTCTGCTGATC
CTGGTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN
TAGGAGATCCCTTTCCCATTCCTC

0978375.101604

FIGURE 176

CTCGCGCAGGGATCGTCCATCGGCCGCGGGCTCGGAGCCGCGACCCCTGGGGGGCTCCGGGATTTGCTACCTTTT
TGCGTCCCTGCTCGTGGAACTGCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCTCTGGCAA
GGAGGGCGAGCCAGGACAGCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTCAGCCGCCAGCCAGCCAGCTG
GCTGTGCTGGGTGCTCCCGAGGCCCTGGCTCTTCTGGGCGAGCGGCGAATGCACCTGGAGCGCTCTTTCGCTGTG
CCCGTTTGAGCCCTGGAGAGACTGACTGCTACAGAGTGGACATCGACAGGGGCTGATATGCAAAAGAAAGCAA
GGAGAACCAAGTGTGGAGTCACTGTTCCGAGCCAGGGCCCTGGGGCAAGATGTTATCTCTGTGCACACGATA
TGAGGCAAGGCGAGGATGGACAGATCTCGAGAGCGGGGATATGATTTGGTCTGCTCTTTGTGCTCAGCCAGTA
CCTTGGCCATCCGGGATGAGTTGGATGGTGGGGAAATGGAAATTTCTGTGAGGACCCGCCAAGGCCATGAAACAAT
TGGGTTCTGCCAGCAGGCGACAGCTCGCCGCTTCTCCCTGATAGCCACTACCTCTTTTGGGGCCCTCAGGAAC
CTATAATTGGAAGGGGACGCGCCAGGGTGGAGCTCTGTGACAGGGCTCAGCGGACCTGGCAACCTCGGACGACGG
TCCCTACGAGGCGGGGGAGAGAGGAGCAGGACCCCGGCTCATCCGGCTCCCTGCAACGACTACTTTTGGCTTT
CTCTATTGACTCGGGGAAAGGTCTGGTGTGCTGCAGAGAGAGCTGAGCTTTTGTGGCTGGAGCCCCCGCGCCAAACCA
CAAGGGTGTGTGTCTCATCTCGCGCAAGGACAGCGCCAGTGCCTTGGTGGCCGAGGTTATGTGCTCTGGGGAGCG
CCTGACCTCGGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGG
TGCCCCCTACTTCTTTGAGCGCCAAAGAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACCAAGGGGGTCACTG
GGCTGGGATCTCCCTCTCCGGCTCTCGGGCTCCCGTGACTCCATGTTTGGGGATCAGCTGGCTGTCTCTGGGGAG
CCTCAACCAAGATGGCTTCCAGATATTGCACTGGGTGCCCTTTTGTATGGTATGGGAAAGCTTCTCATCTACCA
TGGGAGCTGCTGGGGTGTGTGCCAAACCTTCAACAGGTGCTGAGGGGCGAGGCTGTGGGCATCAAGAGCTTCGG
CTACTCCCTGTCCAGGCGACTTGGATATGGATGGGAACCAATACCTGACCTGCTGGTGGGCTCCCTGGCTGACAC
CGCAGTGTCTTTCAGGGCGAGACCACTCTCCATGCTTCCCATGAGGTCTCTATTGTCTCAACGAGCATCGACCT
GGAGACGCCAACTGTGCTGGCGGCACTCGGTCTGTGTGGACCTAAGGGTCTGTGTTCACTCACTTGCAGTCCC
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTAGATGCGGACACAGACCGGAGGCTCGGGGGCCAGGT
TCCCGGTGTGACGTCTCTGAGCCGTAACCTGGAAAGAACCAAGCACAGGCTCTGGGCAACCGTGTGGCTGAAGACA
CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCTCAGCTCCAGGAAAATGTCAAGACAAGCTTCTGGGCCATTGT
AGTGACCTTGTCTTCAAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCTGGCCAGGGGCTGCTCCAGTGGC
CCCATCTCATAGGCCACAGCCAGGACCCAGCGGGCAGAGATCCACTTCTGAAGCAAGGCTGTGGTGAAGA
CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCAGCGCCGCTTCTTACCCGGGTGAGGACACGGAATTCBAAC
TCTGCCCATGGATGGATGGATGGAAACACAGCCCTGTTTGAACAGTGGGCGAGCGACTCATGGCTGGAGCTGAT
GGTCAACCACTGCCATCGGACCGACCCAGCCAGGCTGATGGGGTATGAGGACCGAGCTCTCTGGT
CATGCTTCTCACTCACTGCACTACTCAGGGCTCGGGCCCTGGGACCTCGGAGAGGCCACTCTGCTCTGCCCTCAA
TGGAATGCTCCCTCCATGTTGAGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCAGGTCACTTCTACTCATCT
CCTTAGCACTCCGGGATCAGCATTTGAGACCAAGCACTGGAGGTAGAGCTGCTGTGGCCAGCATCAGTGAGCA
GGAGCTGACTCAAGTCTCTGCAAGAGCCCGTGTCTTCTTAGCTGCTGCCATGTCATGTCAGGAATGGCCATTCC
CCAGCAACTCTTCTTCTCTGTGTGTGTGAGGCGCCAGAGAGCCATGCACTGCGGGGATGTGGGCGACAGGT
CAAGTATGAGTCAAGCTTTTCAACAGGCCAGTGGTGTCTTACCCAAATGCGAGGTGTAGCTGGAGCGGGATCGGCG
GCTGATGAGATTTGCCAATGGGAAGTGGTGTCTGTACCCAAATGCGAGGTGTAGCTGGAGGGCGGGCAGGGGCTGG
GCAGAAAGGGCTTTGTCTCTCCAGGCCCAAACATCTCCACTGGATGTGGACAGTAGGATAGGAGGGCGGGGGA
GCTGGAGCCGACTTGGCAGCAGGAGGCTGTGTGAGCGGAGGAGCCAGCATGTCTGTGTGGCAGGTGTCTCTGCT
TGAGAGAGAAAGAAACATCACCCTGGAATGCGCCCGGGCGAGCGCCAACTGTGTGGTGTTCAGCTGCCCATCTTA
CAGCTTTTGAACCGCGGGCTGTGTGTCATGTCTGGGGCCGTCTCTGGAAACAGCACTTTCTGGAGGAGTACTCAG
TGTGAAGTCCCTGGAGAGTATTGTCTCGGGCCAAACATCACAGTGAAGTCTTCCATAAAGAACTTGATGTCTCGAGA
TGCCCTCCAGATGATCCAGTGTGATTAFTTGAACCCAGTCTGTGGTGGCAGAGGAGTGGCCCTGGTGGGT
CATCTCTCTGTGCTGATGTGCTGGGCTGTGTGTCTAGCACTGTGGTGTGTGTCTCTGTGGAAGATGGGATCTTA
CAACCGGGCGAGGACCCCGGAGGACCCGTGGCCAGTACATGCGGTGAAGATTTCTCGGGAAGACCCAGCAAGCA
GTTCAAGGAGGAGGACAGCGGCCACCTCTTGAGGAAACATGGGGCAGCCCGCGGGGAGGGCCGGATGCA
CCCCATCTGCTGTGACGGGCTTCCGAGCTGGGCGCCGATGGGCTCCCGGCGAGGACCGCGCTTAGGTTT
CATGTCCAGCTGGCTGGCTGTGCTGCGCTCCATCCCTTCCCAAGATGGCTCTTGGATGAAGAGGGTAGAGT
GGGCTCTGTGTGTCATCAAGATTGGCAGGATCGGCTTCTCAGGGGCAACAGCTCTCCCAACCAAGAAC
TCTCTCCACCACTCTCCCTTAGAGTGTGTGAGATGAGATGGGTAATCAGGGAACAGGGCCATGGGGTAGGG
TGAGAAGGGCAGGGGTGCTGTGTCAGAAAGTGGGGAGAGGGATCCTAATCTCTCTCTCCCTTCACTCCCTGT
GTAAACAGGACCCAGGACCTGCTTCCCGGAAAGTGCCTTAACTAGAGGGTGGGGAGGAGGTGTGTGCTGTA
CTCAGGCTGTCTCTCTTAGTTTCCCTCTCACTGACCTTAGTTTGTGCCATCAGTCTAGTGGTGTTCGTGGT

09/18/375.101603

FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPQALALPGQANRTGGLFACPLSLEETDCYRVDIDQGADMOKESKENQWL
GVSVRSQGGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQLDAIRDELDDGGEWKFC
RPGQHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGATARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRLLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSFGFGYSLAVADLNSDGWPDLLIVGAPYFFERQEBELGGAVVYVLNQGGHWAGI
SPRLRCGSPDSMFGISLAVLGDNLNQDGFDDIAGAPFDGDKVFTIYHGSSLGVVAKPSQVLE
GEAVGIKSGYSLSGSLMDGNQYPDLLVGS LADTAVLFRARPILHVSHEVS IAPRSIDLEQ
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDADTDRLRGQVPRVTFLSRNLEEPK
HQA SGT VWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYSLQTPRLRRQAPGQGLPPVAP
ILNAHQ PSTQRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSDTFQPLPMDVDGTTALFA
LSGQPVIGLELMVTNLPSDPAQPPADGDDAHEAQLLVMLPDSLHYS GVRALDPAEKPLCLSN
ENASHVECELG NPMKRGAQVTFYLI LSTSGIS IETTELEVELLATISEQELHPVSARARV
IELPLS IAGMAI PQQLFFSGVVRGERAMQSERDVGSKVYEVTVSNQGGSLRTLGS AFLNIM
WPHEIANGKWL LYPMQVELEGGQPGQKGLCS PRPNILHLVDVSRDRRRRELEPPEQQEPGE
RQEPMSWPPVSSAEKKNI TLD CARGTANC VVFS CPLYSFDRAAVLHVWGR LWNSTFLEEY
SAVKSLEVIVRANI TVKSSIKNMLLRDASTVIPVMVYLDPMVA VAE GVPWWVILLAVLAGLL
VLALLVLL LKMGFFKRAKHPEATVPQYHAVKIPREDRQOFKEEKTGTILRNNGWSPRREGP
DAHPILAADGHPELGPDGHPGPCTA

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

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FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGTCTGGCT
CACACAAGATGCTCAAGGTGTAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTCCGACGGCGGTAATTTTC
TGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAAC
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCGAGTGGTCTATCCAGCCCTGTTTGTGGTTCCAGATGGTCATACCTACTCTTTTCAGTGCA
AACTAGAATATCAGGCATGTGCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC
CCATGTCCTTCAGATAAGCCACAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT
GGAGTTCCAGGGAAGTGGCAAAACAGATTGCGGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAA
GTCAAAAACAAGAAGCAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTGATACCGAGCATC
TTGCCAATTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAAACTATGACCT
GCTATTGGACCAAGTCAGAGCTCAGAAGCATTACCTTGATAAGAATGAACAGTGTACCAAGG
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTGAGAAGCGGCA
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGTCTATGGCAGTGTGGACAGTGTGTTGTGTTGACAGATATGGAAATGAAGTC
ATGGGATCCAGAATAAATGGTGTTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGTGAC
CATGATGTATACATTGATTTGATGACAGTTGAAATCAATAAATCTACATTTCTAATATTTA
CAAAAATGATAGCCTATTTAAATTTATCTTCTCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAAGTTTATGTTTAAAT
AAGAATCATTGTCTTGAAGTTTATATTTCTTACACAAAAAGAAAATACATATGCAGTCTA
GTGAGCAAAAATAAGTTTGAAGTGCTACTATAATAAATTTTTACGAGAACAACTTTGT
AAATCTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAAG
ATAATTCTAAGTGAAATTTAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATGTCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCACATGACTCCAAAAA

FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829
><subunit 1 of 1, 436 aa, 1 stop
><MW: 49429, pI: 4.80, NX(S/T): 0
MLKVSAVLCVCAAAWCSQSLAAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKPFQALDPAKDPCLMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPVVYPSVPCGSDGHTYSFQCKLEYQACVLGKQISVKEGHCPCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSONKKTLLRPERSRFDTSILPI
CKDSLGMWFMRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ
RQQDPPCQTELSNIQKRQGVKLLGQYIPLCDEDDGYKPTQCHGSVGQCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDEDEGDDDDGGDDHDVYI

Important features:

Signal peptide:

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

0978375-101601

FIGURE 180

CAGACTCCAGATTTCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGGC
 CTTCTTCAGCCGGGATCGCCACAGCAGGGATGGGGCGACAAGATCTGGCTGCCCTTCCCGGTGCTCCTTCTGGCC
 GCTCTGCTCCGGTGCTGCTGCTCGGGCGGGCGGCTTCACACCTTCCCTCGATAGCGACTTCACCTTTTACCCCT
 CCGCGCGGCGCAGAAGGAGTGCCTTCTACCGCCCATGCCCTGAAGGCCCTCGCTGGAGTACCAAGTTCTTTA
 GATGGAGCAGGATTAGATATTTGATTTCCATCTTGCTCTCCAGAAGGCAAAACCTTAGTTTTGAACAAAGAAA
 TCAGATGGAGTTACACCTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACATACATTCAGACACCTT
 TCTGAGAAGGTGATTTTCTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAGAACAACAAGAGTTTGAAG
 AAATATATTACTGGGCACAGATATATTTGGATATGAACTGGAAGACATCTCGAATCCATCAACACATCAAGTCC
 AGACTAAGCAAAAGTGGGCACATCAAAATTCGCTTAGAGCAITTTGAAGCTCGTATCGAAACATCAAGAAGC
 AACTTTGATAGAGTCAATTTCTGGTCTATGTTTAATTTAGTGGTCAITGTTGGTGGTCTGAGCCATTCAAGTTTAT
 ATGTCGAAGAGTCTGTTTGAAGATAAGAGGAAAGTAGAACTTAAAACTCCAAATCGAGTACAGTACATTTGAAA
 AATGAGGCATAAAATGCAATAAATCTGTACAGTCAAGACCATTAAATGGTCTCTCCAAAATATTTTGAGATATA
 AAAAGTAGGAAAACAGGTATAATTTTAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCTCGCTGATCCAG
 TTGTACTTAAGTGTGTACAGGGAATTTTGCGAATATAGGTTTAACTGAATGAAGCCATATAATTAACATGCAT
 TTTCTCAACTTTGAAAAATTTTGCAAAATGCTTAGGTGATTTAAATAAATGAGTATTTGGGCCAATTTGCAACACC
 AGCTGTGTTTAAACAGGTTCTATTAACCGAACCTTTTGTAAATCGCGCAGTTACAAATTAACGTGGAAGTTT
 TCAGTTTAAACAGGTTCAATCACTGAGAAATTAACCTAATGATGGATTGAATAAATGAGTATTTGGGCCAATTTGCAACACC
 CTTTCTCTATTTACATATGTCATCTCTCTATAATGTAATAGAAATAAGCTTTGAAATACAAATAGGTTTGTG
 AGATTTTATAACCAATACATTTCAAGTGAACATATTAGCAGAGAAGCATTAGTCTTTGTATCTTTGCTTACATT
 CCAAAAGCTGACATTTTCAAGATTCTTAAAAACAACAAGTTACACTTACTAAAATTAGGACATGTTTCTCTTG
 AAATGAAGATATAGTTTAAAGCTTCTCTCCATAGGGACACATTTTCTCAACCTTAACTAAAGGTAGGA
 TTTTAAATTAATAGTGTAGGATAAATAAGTTTATTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA
 TAATCAAGTTATGTTAAATTTTAAACATGATTTGCTGACTTGGATAATTCATTATCCAGCAGTTATGAAGGAATA
 TTGCTAAATAGTCTGGGCCCTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTTATCAGAAAACAGGAA
 AGAATTTAGAAAACCTTGAGAAAACCTAATCCAAAATAAAATTCATTAAGTAGAATATAAAATAATATCTAGA
 ATCTGACGTGCTCATCATGACCTCCTACTCATAACTAAATCAAGGAGATGATTAATTTCCAGTTAGCTGGAAG
 AAACTTTGGCTGTAGGTTTATTTTCTCAAGAATTTCTGGTTTGAATTTTATTTGTAAGCAGGTACATTTTATA
 AAATGTGAAGCCCTACTGTAAAGTTTAGCACTGGGTGTACATATTTATTAATAATTTTATATAACAATTTTAT
 TAAATGGCCCTTTCTGAACCTCTTATTTATTGATGTGAAGTAAAGGATTGAATAACATGATCTGTTTAT
 CACCTAAATGTGAATAACCCATATATAACAAGAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGTCTTAC
 TCAAGTACTAGTAAATTAACCTCATCATGAATGAATATAAATTTGGGGTATAGAACCCTCAACAGGTTAGATATGCTGGAAT
 GACTACATTTGAGTTAGAAAACAAATTTGAGGTTATAGAACCCTCAACAGGTTAGATATGCTGGAAT
 CTTGATGAGCAATATGATTAACAGAGAGTGATTTCAITTAACCTCATAGTAGTATAAAAGACAGATATTTCCCT
 TCTTAGGCCCTGGGAGAAAGAGCAGCTTAGATTTCCCTACTGGCAGGTTTAAAAATGAGTAAATGCCGAT
 ATGATCAATTAACCTTAATTTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCTCTGCAACACTGCAAGAACAA
 AGGTCAATAAGATCCTTGCCATGAATACCCCTCCCTTTTGCGCTGTAAATTTGCAATGAGAAGCAAAATTTACA
 GTACCAATACTAATAAAGCAGGGTACAGATATAAACTACTGCATCTTTTCTATAAACTGTGATTAGAATTTCTA
 CCTCTCCTGTATGGCTGTTACTGTACTGTACTCTCTGACTCCTTACCTAACCAATGAATTTGTTACATAAATCTT
 ACATGTATGATTTTGCCACTGATCTTAAACCTATGATTCAGTAACCTCTTACCATATAAAACAGATAATTTGCTT
 TATTTGGAAGAAATTTAGGAATATAAAGGCAATTAATTTTATAGCAAAAGTAAAAAGACAGATATTTAAGAGG
 CATTAACCAAAAAGCAAACTGTAAACAGAGTAAAAATCTTAAATATTTTAAAGACATACCTGTTTATCTGCTT
 CATATGCTTTTAAATTTCACTATTTCCATTTCTAAATTAAGTTATGCTAAATTTGAGTAAGCTGTTTATCATCT
 AACAGCTCATTTTGTCTTTTCAATATACAAATTTTAAAAATACCTACATAATTTAACTAAGGCCCAACCGATTTC
 CATATTTAGAGCATACCGTGTACCTTCACTCACTAAGGCCCTAGAGTTTGTCTGATATGCAITTTGGATGATTTAT
 GTTATGCTGTTCTTTCATGTGAATGTCAAGACATGGAGGGGTGTTGTAATTTATGGTAAATTAATCCTTCTTA
 CACATAAATGGTGTCTTAAATTTGACAAAAATGAGCATCTAACATGTATGTTCTCTCCAAAGGAAGATTTCTTAT
 GTGAAATTTAAAGACATTTGATTCGCATGTAAGGATTTTTCATCTGAAGTACATATAAGCAACATCAGTGTG
 CTCAACTGCTTTATACTTATAAACAGCCATCTTAATAAGCAACGATTTGTGAGTATGATATGATATAATAA

FIGURE 181

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196
><subunit 1 of 1, 229 aa, 1 stop
><MW: 26017, pI: 4.73, NX(S/T): 0
MGDKIWLPFPVLLLAALFPVLLPGAAGFTPSLDSDFTLPLAGQKECFYQPMPLKASLEIEY
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFPEL
ILDNMGEQAQEQEDWKKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN
IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

0978375-701601

FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCCAGTGTCTCCTGGATG
CTGCTTTCTGCCTCATTTCTCCTGTGTCAAGGTCAAGGTGAAGAAACCCAGAAGGAACTGCC
CTCTCCACGATCAGCTGTCCCAAAGGCTCCAAGGCCATGGCTCCCCCTGCTATGCCTTGT
TTTTGTACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTGATGATCCTCC
TTCTTTTCTCTTTTCTTACCTTCATTTAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC
TCAGAGAATAATAATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

0978375.101601

FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIWGLHDPDQSEPDGDGWEWSS
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

097875.101601

FIGURE 184

CCAGTCTGTGCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGTGCTGGC
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGA CTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCTGTCTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTGTTAGAGTCCCCGCCCACCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

0976375.101601

0963-7461

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405
```

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP

FOGDSTVTKSCASKCKPSDVDGIGOTLPVSCCNTEL CNVDGAPALNSLHCGALTLLPLLSRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGG
ACGGTTTTCTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTCTCCCTCTT
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG
TAGCGGCGGCTCTCGGGCGCCACCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTCTC
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGACCCAGGCTC
TGCACTCAGCGCCGCGCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGACGAGGCGTGCAAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAAAG
CTGCATGCGTCACGCTATGTGCTGCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGGTATTTCAGAAGAACCACCTTGCTCTTCAAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCTTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTCT
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTGTGCAGA
GACACTAAACCAGCTATCCAAATGCAGTGAACTCCTTTTATATAATAGATGCTATGAAAAAC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCCTG
TGATTGCAGTAAATTAATGTATTGTAAATCTCAGTGTGGCACCTACCTGTAAATGCAATGA
AACTTTTAATTATTTTCTAAAGGTGCTGCACTGCCTATTTTTCCTCTTGTTATGTAAATTT
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT
TCAGCTTATAGTTCTTAAAAGCATAACCCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA
AGGATCTCTTGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA
AATAAAATTTAACATTTAAAAA

0978375.101001

<subunit 1 of 1, 266 aa, 1 stop

MMALGAAGATRVFVAIVAAALGGHPLLGVSATLNSVLNSNAIKNLPPLGGAAGHPGSAVSA
APGILLYPGGNKYQTIDNYQPPYCAEDDEECGTDEYCA5PTRGGDAGVQICLACRKKRKRMRH
AMCCPGNYCKNGICVSSDQNHFRGEIETITESFGNDHSTLDGYSRRTTLLSSKMYHTKGQEG
SVLCRRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHKRKGSHGLEIFQRCYCEGGLSCLRIQ
KDHDOASNDSSRLHETCORH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTTCTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTTGTNGCGATG
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCCGCGCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCANGCTATGTGCTGCCCCGGAATTACTGAAAAATGGAATATGTGTGNTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG

0578375-101601

FIGURE 189

GAGGAACCTACCGGCTACGGCGCGCGCTGGTAGTCGCGCGGTGTGGCTGCACCTCACCAATCCCCTGCGCGCGGG
 CTGGGCCCTCGGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTGGGCTCGGCCAGGCGGGGCTCGCCGCCA
 GGGTTTACGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAGGA
 AGTATTTAGAAATGAGCTGAAGACCATTCACAGATTAAATTTTTTGGGGACAGATTGTGATGCTTGATTCACTCT
 TGAAGTAAATGTAGACAGAAAGTTCTCAAAATTTGCATATTACATCAACTGGGAACAGCAGTGAATCTTAATGTCTAC
 TTAATACGAATCTTGCAATAGAAAGAGAATGGGAGTCTGGTTAAATAAGAGTACATATTACAGACATTTGAAAG
 GATCATTTCTCTGTTTTCTGTATGTGTATATGGCCATTTTTAGTGGGACAGATCAGGATTTTTTACAGTTTACTTGG
 AGTGTCCAAAATTCGAAGCAGTAGAGAAATAGACAAGCTTTTCAAGAAATTTGGCATTTGAAGTTACATCTGATA
 AAACCCGAAATACCCAAATGACATGGCGATTTTTTAAAAATAAATAGAGCATATTGAAGTACTCAAGATGAAGA
 TCTACGGAAAAAGATATGACAAATATGGAGAAAAGGGAATTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA
 CTATTATCTGTTATGATTTTTGTTATTTATGATGATGATCCTGAAATCATAACTTGGAAAGAGAGAATTTTTGATGC
 TGCTGTTAAATTTCTGGAGAAGTGTGGTTTTGATAAATTTTTTACTCCCAGGCTGTTTCACACTGCCATGATTAGCTCC
 CACATGGAGAGACTTTTGCTAAGAAAGTGGATGGGTTACTTCGAATTTGGAGCTGTTAACTGTGGTGATGATAGA
 GCTTTGCGGAATGAAAGGAGTCAACAGCTATCCCAGTCTCTTCATTTTTTCGGTCTGGAATGGCCCGCATGAAATA
 TCATGGAGACAGATCAAAAGGAGATTAGTGAGTTTTTGAATTTGCAATGCAGCATGTTAGAAAGTACAGTGACAGAACTTTG
 GACAGGAAATTTTGCACTCCATCAACAACTGCTTTTTGCTGCTGGTATGGCTGGCTGATCACTTTTTTGTTCAAA
 AGGAGGAATTTGTTGACTTACAGACACGACTCAGGCTTAGTGGCATGTGTTTTCTCACTCATTTGGATGTAAAA
 AGAAATATATTTGGAAGTAAACATATCTCCAGATTTTGAAGTACTTTTCGGCAACACACTAGAGGATCGTTT
 GGCTCATCATCTGGTGGCTGTTATTTTTCAITTTGGAAAAATGAAATTAAGATGCTGAGCTGAAAAAACT
 AAAAATCTGCTTTAAAAATGATCATATCTCAAGTTGGCAGGTTTGAAGTGTCTCTGACACAGACATCTGTAGTAA
 TCTGTATATTTTTTCAAGCTCTCTAGCAGTATTTAAAGGACAAAGAACATAGAAATTCATCATGGAA
 GAAGATTTATATATGATATACCTTGCTTTGCAAGAAAGTGTGAATTTCTCATGTTACACAGCTTTGGACCTCAAAA
 TTTTCTCGCAATGACAAAGAACCATGGCTGTGATTCTTTGCCCCCTGTTCCAGCATGTGCGAGCTGTAACT
 ACCAGATGTTACGAAGAGCATCAATCTTTTATGGTCAGCTTAAGTTTGGTACAGCTAGATGTACAGTTTCATGA
 GAGTCTGTGAATCTGTATAAATCTCAGGCTTATCCAAACAGCAGTGTATTCAACGATCCAACATTCATGAGTA
 TGAAGAGACATCACTCTGCTGAAACAAATCTTGAGGTTTCATAGAGGATCTTATGAACTCCTTCAGTGGTCTCCCTTAC
 ACCACCACTTTCAACGAATCTAGTTACAAAGAAACACACAGCTGTTGAATGGTGTGTTTCTATTCTCCGTG
 GTGATCTCCTTGGCAAGCTTAAATGCCAGAAATGGAAAGAAATGGCCCGGACATTAATCTGAGCTGATCAACGTGGG
 CAGTATAGATTGCCAACAGTATCTTTTTTGTGCCAGGAAACGTTCAAAGATACCTGAGTAAAGTTTCAACAAG
 TCCCCCAAATCAAAATAAGCTTATCAGTATCAAGTTCAAGTGTGGAATAGGAGTCTTTTCCCTGAGAAT
 CTGGGGTCTAGGAATTTTTACTCCTCAAGTATCCACAGATCTAACACTCAGACTTCAGTGTGAAATGTTTCAACAGG
 GAAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGTGGAGCTGCCAGAAATTTTGGCTCAGAAATTTGAGCT
 CTGGCTAGGATGATTAAAGGAAAGTGAAGGCTGGAAAAAGTAGACTCAGGCTTATGCTCAGACATGCCAGAA
 AGCTGGGATCAGGGCTATCCAACTGTTAAGTTTTATTCTACGAAGAGCAAGAGAAATTTCTCAAGAACAGCA
 GATAAATACAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAATAATTTGGAAATCTCCGAATCAAGGCCA
 GAGGAATAAGGATGAACCTTTGAATAATGTTGAAGATGAAGAAAAAGTTTAAAGAAAAATCTGCAGAGATGACATCAG
 AAGACACCTATTTAGAATGTACATTTATGATGGGAATGAATGAACATATCTTAGACTTCGAGTTGTACTGCCA
 GATTTATCTACAGCATCTGTTGTAAAGAGAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTTATAAATATTTTA
 GACTTTGCAAGCTATAATATATGTTTCAACATGAGAACAAAGATAGAGTCATATGTTATCTTTGTTATTTGCT
 TTTAACAACTTTTAAAAAATATTAAACGATCTTAGCTCAGAGCCATACAAAGATAGGCTGGATCAGTCCAGT
 GACCATGATTTGCTGTGCCCCCTGACGGACTTATAATGTTTCAAGTGGCTGGCTGAACTAGTCTGCTGCTGCT
 ATCTACATAAATGTCTAAGTTGTATAAAGTCCATTTCCCTCTACGTTTTTGGCTGACCTGAAAGAGGTAAC
 TAGTTTTTGTGCTGTTCTCTTAAAAATGCTATCCCTAACCATATTTATATTGTTTTTAAAAACCCCAT
 GATGTGGCAGCTGATTAACAAACCTGTTATGCTGATATATATGAGGAGATTTCTCATTTGTTCTTTCTCTTCA
 AAGTTTGAAGAAATGCTTTTTAATTTTTTCAAGCCGAGAAACAGTGCAGCAGTATATGTCACACAGTAAGTACAC
 AAATTTGAGCAACAGTAAAGTGCAAAATCTGTAAGTTTGGCTGATCATCCAGGAAGCTGAGGGAAAAAATTA
 TAGCAATTAATCTGGGATGTAGAGATCTCTAAATATGTTATCAAGTATTAGAGTCTATATTTTAAAGATATA
 TGTGTTCATGATTTTCTGAAATGCTTTTCATAGAAATTTTTCCCATGATAGTTGATTTTTGAGGCATCTAATAT
 TTAATCATTTGGCTCTGAACTTTGTTTGAAGCTGATCTCTTTATTTACATTTGGTTTCTTTCTATAGTTTGG
 TTTTTCACTCTGCTCAGTCTATTATTTCAATAGGAAAAATTTACTTTACAGTTGTTTTCATGAGCTTAT
 AATGATATCTGTAGTTATTCCAGTTACTAGTTTATCTGTCAGAGGGCTGCTTTTTTCAGATAAATTTGACATAA
 ACTGAAGTTATTTTTATAAGAAATCAAGTATATAAATCTAGGAAGGATCTTTCTAGTTTCTGTGTTGTTTGA
 CTCAAAGAAATCACAAAATTTGTCAGTAACTGTAGTTGTTTAGTTATAATTCAGAGTGTACAGAAATGTAATAAAT
 CCAATCAGTCAAAAGAGTCAATGAATTTAAAGGCTTGCACTTTTTCAAAAAA

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FIGURE 190

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIIDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL
HPDKNPNPNNAHGDFLKNRAYEVLKDEDLRKKYDKYGEKLEDNQGGQYESWNYRYDFGI
YDDDEPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRMLCRMKGVNSYPSLFI FRSGMAPVKYHGDRSKESLVSFAMQHVRSVTVELWTGNFVNS
IQTAFAGIGWLITFC SKGGDC LTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN
TLEDRLAHHRWLFFHFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLVYFQP
SLAVFKGQGTKEYEIHGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWC
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHHS
AEQILEFIEDLMNPSVVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART
LTGLINVSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG
FLPQVSTD LTPQTFSEKVLQGKNHWVIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDC
QAYAQTQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGKRKNKDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

0078375.101601

FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA
GCCATGAACATCATCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCTACTTGGGA
GTCGTTGGTGAAGTTTTTCATTCTCTCAGAGGAGAAAAATCTGTGGCTGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCCTAGGACATTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCAGAAGGGATTCCCTTACCTCATCCCATAT
TGTTCCAGCAAATTTGCGCGTGTGGCTTTTCACAGAGGTCTGCATCAGAACTTCAGGCCTT
GGGAAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTTGTGAATACTGGGTTACCA
AAAATCCAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA
GATGGAATACTTACCAATAAGAAAATGATTTTTTGTTCATCGTATATCAATATCTTTCTGAG
ACTACAGAAGTTTTCTTCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT
TTGAAGCAGTGGTTGGCCACAAAATCAAATGAAATGAATAATAAATAAGCTCCAGCCAGAGATG
TATGCGATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTACATTTTT
TCAGTCTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA
ATTACCTGTCTTCTGTTTTCTCAAGAATATTTACGTAGTTTTTCATAGGTCTGTTTTTCTCT
TCATGCCCTTTAAAACTTCTGTGCTTACATAAACATACCTTAAAGGTTTTCTTTAAGATAT
TTTTTTTTTCCATTTTAAAGTGGACAAAAGCTACCTCCCTAAAGTAAATACAAAGAGAACT
TATTTACACAGGGAAGGTTTAAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTAAGATTGAGCATTTGAAAGATTTCCCTAGCCTCTTCTCTTT
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACCAAAAGTGGACCTCTATATTTTAAATCTCAGAAATTTAAGTTCTAGCCCCATGA
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAAATTTAAGTTCTAGCCCCATGA
TAACCTTTTTCTTGTGAATTTATGCTTTTATATATCTCTGGTCCAGAGATGTTTAGACAAT
TTTAGGCTCAAAAATTAAGGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA
CAATGGACCCAGAGAAGAA

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FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI
LVLWDINKRGVEETAACRKLGVTAHAYVVDCSNREEIYRSLNQVKEVGDTVIVVNNAGTV
YPADLLSTKDDEITKTFEVNILGHFWITKALLPSMMERNHGHI VTVASVCGHEGIPYLIPYC
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLWPVLETDEVVRSLLD
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

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FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGT'TCCCAGCAGG
ATGCCCCGCTCT'GCGAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGGCCAGCCCGCCCGGGGC
AGGATGACCAAGCCCCGGCTGTTCCGGCTGTGGCTGGTGTGCGGTGCGGTGTTTCATGATCCT
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCT
CTAGGCCGCACACGGGGCCGCGCTGCCACGCCCCGGGCCGGACAGGGACAGGGAGCTCACG
GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCCAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCAGCGCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAATCCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCCAAGGTGGCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGCTGCACCGCGGTGCGCCTACCGCGACCGCTGCGCATCCCGCGCGAGCA
CGTGCAACAACGCCAGCGCGCACCTGACCTTCAACAAGTTTCTGGCGCGCTACGGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTTCGTGCGGACCCC
TTCGTGCGCCTGATCTCCGCCCTTCCGACGAAAGTTTCGAGCTGGAGAACGAGGAGTTCTACCG
CAAGTTTCGCGTGCCCATGTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGC
GCGAGGCCCTTCGCGCTGCGCCTCAAGGTGTCTTTCGCCAATTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCGCGCG
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTTCGCCAAGATCCCCCTGGCCTGGAGGCGAGCAGT
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACTCTCTCC
GAGACTGAAAGCTTTCGCGTTGCTTTTCTCGCGTGCTTGAACCTGACGCACGCGCACTCC
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCCTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAAATATATTTCAGGTATTTAATACGA

0973375-10601

FIGURE 194

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSAFVFMILLIIIVYWDSAGAAHFYLHTSFSRPHPTGPPLPTPGPDRDRDELTA
DSDVDEFLDKFLSAGVKQSDLPKETEQQPPAPGSMEESSVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFFPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRMIVLS
GSLLRHGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAQLQLQLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

0078375-101001

FIGURE 195

TCGGGCCAGAATTCCGGCACGAGGCGGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAAGAGGCCCAGAGTAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTCTGTGACCGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC
GCCTTCGTGAACAGCGGGGCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGTGTGACTCAGGAAGATGATG
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTGGCCGCCTGGATTGTGTTGTCAACAAC
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCTACCTGCGGA
AGAGTCAAGGGAATGT CATCAACATCTCCAGCCTGGTGGGGCAATCGGCCAGGCCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCAGGAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCTAGGGCCACAATCCGAGAGGGCATGCTGGCCAG
CCACTGGGCCGCATGGGCCAGCCCGCTGAGGTGCGGGCTGCGGCAGTGTTCCTGGCCTCCGA
AGCCAACTTCTGCACGGGCATTGAAGTGCTCGTGACGGGGGTGCAGAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGCACCCCGTGACGCCCCGATATCCCTTCCTGATTTTCTCTCATT
CTACTTGGGGCCCCCTTCTAGGACTCTCCACCCCAAACCTCCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCAGTTAGCAAGGTGCCGGGTACCCCTGCAGGTTCCCAT
AAAAACGATTTCGAGCC

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FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTGGGRGIGAGIVRAFNNSGARVVICDKDESGGRALEQEELPGAVFILCD
VTQEDDVKTLVSETIRRFGRLLDCVVNNAGHHPPPQRPEETS AQGFRQLLELNLGTYTLTKL
ALPYLRKSQGNVINISLVAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAVFLASEANFCTGIELLVTTGG
AELGYGCKASRSTPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

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FIGURE 197

AGGCGGGCAGCAGCTGCAGGCTGACCTTGACAGCTTGGCGGAATGGACTGGCCTCACAACTG
CTGTTTCTTCTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA
GAGGAAGGGGCAAGGGCGGCTGGGCCCTGGCCCTGGCCCTCACCAGGTGCCACTGGACC
TGGTGTCACGGATGAAACCGTATGCCCCATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCCACTGAGGAACAGCTCAGAGCTGGCCAGAGAAAGTGTGAGGTCAACTTGCAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCAGCC
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCTGTGTCTGGGCTGTGTGAACCCCTTCACC
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCTGTGCGCCGCCG
CCTCTGCCCCCACC GCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCAGAAAGCCAGGCCAGCAGCCCGAGA
CCATCCTCCTTGACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA
GCAAG

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FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRI PVDLPEARCLCL
GCVNPFTMQEDRSMVSPVFSQVPVRRRLCPPPPRTGPCRQRAVMEITAVGCTCIF

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCTTGA AAAAACC CGGCGGG
CGAGCGAGGCTGCGGGGCGGCGCGCTGCCTTCCCCACACTCCCCCGCGAGAAGCCTCGCTCG
GCGCCCAAATGCGGGGTGGGCGCTGCGGCCCGCAGCTAACGGGCGCTCCTGGCCGCTGGAT
CGCGGCTGTGGCGGCGACGCGCAGGCCCGCAGGAGGCCGCGCTGCCGCGGAGCAGAGCCGGG
TCCAGCCCATGACCGCCTCCAAC TGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATT CAGAATGGGAGGCTTTTGCAAAGAA
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCAATTCAAGAACCGAGTTTGAATG
GCCGCTTCTTTGT CACCAC TCTCCAGCATTTTTCATGCAAAGGATGGGATATTCGCCGCT
TATCGTGGCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC
TTTTAGCATCTCTGGCAAGATATGGCATCTT CACAAC TATTT CACAGTGACTCTTGGAATT
CCTGCTTGGTGTCTTATGTGTTTTCTGTCATAGCCACCTTGGTTTTTGGCCTTTTATGGG
TCTGGTCTTGGTGGTAAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCGAGGATGCGGAG
GAGGAAAAAGATGATTCAAATGAAGAAGAAAA CAAAGACAGCCTTGTAGATGATGAAGAAGA
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGCAACTTGGCTG
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCAGGAGAGGACGGTGTG
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCCTGCCAGC
TGACACAGAGGTGGTGGAAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGTGCAAGAGGAC
TG TAGATTAAATGATGGTTTTCAAGAATACACACCAAACAATATGTCAGCTTCCCTTTGG
CCTGCAGTTTTGTACCAATCCTTAATTTTTCTGAATGAGCAAGCTTCTTTAAAGATGCT
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATATAAGGAGAGTCTTCCAGGTGT
GACAATCAGGATATAGAAAAACAACGTAAGTGTGGGATCTGTTTGGAGACTGGGATGGGAA
CAAGTTCATTTACTTAGGGGTCAGAGAGTCTCGACCAGGAGGACCAATCCAGTCCCTAATC
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAGCCAAGCAGGAGCCTTGGCT
CCTGAGCATCCCCAAAGTGTAACTGAGAAGCCTTGATCCTTTTCTGTGTAAAGTATTTAT
TTTTGTCAAATTGCAGGAAACATCAGGCACCAAGTGATGA AAAATCTTT CACAGCTAGAA
ATTGAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCAGCCCTCTGAATCTCCTG
TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCCACCATGGGCATTCAGGCTCT
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC
TGTGTTTGTTCATTTCTGACCTAAGGGGTTTAGATAATCAGTAACCATACCCCTGAAGCTGT
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT
TTACAGACAGATTAAAAAAAATGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTTT
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCCTAAGTCTTGCCAGTACAAGGTAGT
CTGTGGAAGAAAAGTTGAATACTGTTTTGTTTTCACTCAAGGGGTTCCCTGGGTCTTTGAAC
TACTTTAATAATACTAAAAACCACCTTCTGATTTTCCTTCAGTGATGTGCTTTTGGTGAA
GAATTAATGAATCCAGTACTGAAAGTGAAGATTTGATTTTCTCATCTTCTGTAATC
TTCCAAAGAAATTATCTTTGTAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG
GCTAATTTCTTT

05975375.101601

0 **9** **8** **7** **6** **5** **4** **3** **2** **1**

<subunit 1 of 1, 349 aa, 1 stop

MAGGRCGPQLTALLAAWIAA VAATAGFEEAALPPBQSRVQPMTASNWTLVMEGEWMLKFYAP
WCPS CQQT DSEW EAF AKNGEILQISVGKVDVIEPGLSGRFFVTTLPAFFHAKDGI FRRYRG
PGIFEDLQNYIILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKLIWHLHNYFTVTLTGIPAW
CSYVFFVIATLVFGLFMGLVLVVISECFYVPLPHRLSERSEQNRRSEEAHRAEQLQDAEEK
DSDNEEENKDSLVDDEEKEDLGDEDEAESEEEDNLAAGVDEERSEANDQGGPEDGVTR E
EVEPEEAERGIS EOPCDEATTEVVSDSLRORKSHADKGL

Signal peptide:

Transmembrane domain:

N-glycosylation site.

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTGTGTTAAACTCCGGTAAGTACCTAGCCCATGATT
 TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC
 CAAATGCTATATCTATTTCAGGGGCTCTCAAGAACAAATGGAATATCATCTCTGATTTAGAAAAAT
 TTGGATGAAGATGGATATATCTCAATTACACTTCGACTCTCAAAGCAATACCGGATAGCTGT
 TGTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCCCTCATTGCTGTAATTTTGG
 GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCTTGGGTACCATGGGGGTTCTTTCC
 AGCCCTTGTCTCCTTAATTGGATTATATATGAGAAGAGCTGTTATCTATTGAGCATGTCACT
 AAATTCCTGGGATGGAAGTAAAAGACAAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG
 ACAGCTCAAATGAATTGGGATTATAGTAAAACAAGTGTCTTCCCAACCTGATAATTCTATTT
 TGGATAGGCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
 CTCTTCTAATCTATTTTCAGATCAGAACCACAGCTACCCCAAGAAAACCATCTCCAAATTGTG
 TATGGATTACAGTGTGAGTCATTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT
 GAGAAGAAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA
 AGGAGGACAGAAAAACAGAACAGAAAAAGAGTAACAGCTGAGGTCAAGATAAAATGCAGAAAAATG
 TTTAGAGAGCTTGGCCAACTGTAATCTTAAACCAAGAAATGGAAGGGAGAGGCTGTGATTTCT
 GTATTTGCGACCTACAGGTAGGCTAGTATTATTTTCTAGTGTAGATCCCTACAGCATGG
 AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTATTTTTTGTAGATAGGGTCT
 CACTTTGTATACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC
 CTCAGCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTTGGTG
 TTTTTGTAGAGACTGGGTTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCTCGGCTTAAAG
 TGATCTGCCCGCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC
 CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTACCTTGGGTAAGCCATAAGCGA
 ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT
 GTGTGCCACGATTTGACCCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAT
 ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAATCTTACCACAGTCAGAGCAATTTT
 ATTATTTTCATCAGTATGATCATAATATGATTATCATCTTAGTAAAAAGCAGGAACCTCTA
 CTTTTCTTTTATCAATTAATAAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT
 TTTTTTTTTTTTTTTTTTGTAGACAGAGTTTCGCTCTTGTGTGCCAGGCTGGAGTGCAACGG
 CACGATCTCGGCTCACCGCAACCTCCGCCCTCGGTTCAAGCAATTCCTCGCTCAGCCT
 CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTGTAGT
 AGAGACAGGGTTTCTCCATGTGCGTCAAGGTAGTCCCGAATCTCTGACCTCAAGTGATCTGC
 CTGCCCTCGGCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT
 TGTATAATATGTAATGTAGGGAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA
 AAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA
 ACAAGTATTAACATTTTGGAAATAGTTTTATAGTTTTGTGATGATGTTTTTACAATTTT
 ACCATTTTTTTCAGTAATTTACTGTAAAATGGTATTATGGAATGAACTATATTTTCTCATG
 TCGTGATTTGTCTTATTTTTTTCATACTTTCCCACTGGTGCTATTTTTTATTTCCAATGGATA
 TTTCTGTATTACTAGGAGGCATTTCAGTCCCTAATGTTGATTAATATGTGAAAAGAAAT
 TGTAACCAATTTTACTAAATATGCAAGTTAAAATGGATGATTTTATGTTATGTGGATTTCAT
 TTCATATAAAAAAACTCTTATCAAAAAA

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050725Z

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912
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<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDDGYQLHFDQSNSNTRIAVVSSEKGSCAASPPWRLIAVILGILCLVLIVIAV
VLGTMGVLSSPCPPNWIIEYKSCYLFMSLSNSWDGSKRQCWLQGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

FIGURE 203

GGAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCAGACCTGGAGGGTCTCGCTCTGTCA
CACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATGTAACTCCACCTCCCGGGTTCAAGTGAATTCATCTGCC
TCAGCTCCCGAGTAGCTGGGATTCACAGGTGGTGAATTCACAGAGTGACTCCGTCGGAGGAATATGACTCTCCAG
TCTGCTGCTCAGACGACACTGTCTTCTGCTGAGTCTGTCTTCTCTGGTCCAGGTGCGCCAGCGGAGGGGCCACAG
GAGACTTTCCTGCTCTGTCAGCCAGCGGAACACAGACACAGGAGCAGCTTCCACTACAAACCCACACAGAGCTTG
CGATCTCCATCCAGAAATCTCCAGAGGCCCCCTACAGTTCATGCCCCCTTTCCCTGCAGCCCACTTCTCTCCGA
TCCTTCCCTGACCCCAAGGGGCTCTACACCTTCTGCTCTACTGGAACTGCAGTCTGGAGATTCATCTTCTC
TATGGCACAGCTGACTTCTTGTCTGAGTGACAAGGCTCTAGCTCTCTCTGCTCTCAGCAGCAGGAGGAGGCTCT
GCTCAGGGCCCCCGCTGTTAGCCACTTCTGTCACTCTCTGGTGGAGCCCTCAGAAACATCAGCTTCCAGTGGC
CGCAGCTTCACTTCTCTCTTCCACAGTCTCTCCACAGCGCGCTCACAATGCTCTCGGTGAGCATGTGCGAGCTG
AAAAGGGACCTCCAGCTGCTCAGCCAGTTCCTGAAAGCATCCCGAAGGCCCTCAAGGAGGCCCTCGGGTCCGCC
GCCAGCCAGCAGTGTGAGAGGCTGGATCGAAATGACCTCTGTGAGATTTCATGGGGGACATGGTGTCTCTCGAG
GAGGACCGGATCAACGCCACCGTGTGGAAGCTCCAGCCACAGCGGCTCCAGGACCTGCACATCCACTCCCG
CAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACTCTTCCAGAGGACGAAAGGC
CGGAGCGGGGAGGCTGAGAGAGACTCTCTCTGTGGACTTCAGCAGCCAGGCCCTGTTCCAGGACAAGAAATTC
AGCCAACTCTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAAACACAAAGTAGCAACCTCAGGAGCCCGT
GTGCTCACTTTCAGCACAGCTACAGCCGAAAGATGTGACTTGTGCAATGTGTGTTCTGGGTGAAGACCCACA
TTGAGCAGCCCCGGGAGCTTGGAGCAGTGTGGGTGTGAGACCGTCAGGAGAGAAACCAAACATCTGCTCTGCTC
AACCACCTTGACCTACTTCTGATGCTGCTGATGCTCTCTCGGTGGAGGTGGAGCCGTCGACACAGCACTACTGGAGC
CTCTCTCTTACGTGGGCTGTGTGCTCTCTGCCCCGCGCTGCTTGTCAACATTGACGCCCTACTCTCTGCTCCAGG
GTGCCCTCGCGTCAGGAGGAACCTCGGAGTACACCTCAAGGTGACATGCGCTGAGCTGTGCTGCTGCTCTTCT
CTGCTGGACAGAGCTTCTGCTCAGCGAGCCGCTGGCCCTGACAGGCTCTGAGGCTGGCTGCCAGCCAGTGGC
ATCTTCTGCACTTCTCCCTGCTCACTGCTCTTCTGGATGGGCTCGAGGGGTACAACTCTACCGACTCGTG
GTGGAGGTCTTGGCACCTATGTCCCTGGCTACTACTCAAGCTGAGCGCATGGGCTGGGGCTTCCCATCTTT
CTGGTGAAGCTGTGGTGGCTGTGGATGTGGACAACATATGGCCCCATCATCTTGGCTGTGATAGGATCCAGAG
GGGTGATCTACCTCTCCATGTGCTGGATCGGAGTCTCTGCTCAGCTACATCAGCAACCTGGGCTCTCTCAGC
CTGGTGTCTTCTGTTCAAACATGGCCATGCTAGCCACCATGGTGGTGCAGATCTCGGCTGCGCCCCCACCCCAA
AAGTGTGTCACTGTGCTGACCTCTGGGCTCAGCCCTGCTTGGCTGCGCTGGGCTGTGATCTTCTCTCTCC
TTTGGCTTCTGGACCTTCCAGCTTGTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
TCTCATCTGTGATGTGCTGCGGCTGAGGCCCGGGGTGGCCCCCTCCCTCTTGAAGAGCACTCAGACAGCGCC
AGCTCCCATCACTGCTCCGCGACACTCTGTCACCGCATCTAGGCTCCAGCCCACTGCCATGTGATGAAG
CAGAGATGCGGCTGTGTGACACATGCTGTGGCCCCGAGCCAGGCCCAAGCCCAAGCCAGCTCAGCGCAGACT
TTGAAAGCCCAACGACCATGAGAGATGGGCGGTGGCATGTGGAGCGACTCCCGGGCTGGGCTTTGAAATTG
GCTTGGGGACTACTCGGCTCTCACTCAGCTCCACGGGACTCAGAAGTGGCGGCGCATGTGCTCGCTAGGGTACTG
TCCACACATCTGTCCCAACCCAGCTGAGGCTGTGCTCTCTTCAACCCCTGGGCCAGCCCTCATTTGCTGGG
GGCCAGCCCTTGAATCTTGAGGCTCTGGCACATCTTAATCTGTGGCCCCCTGCTGGGACAGAAATGTGGCTCA
GTTGCTCTGTCTCTGTGTGCTCACTTCACTGAGGCACTCTGATCTCTGTCTATTTAACTCTAGGTGGCACCCAGGG
CGAATGGGGCCAGGGCAGACTTCAAGGCCAGAGCCCTGGCGAGGAGAGGCCCTTTGGCCAGGACACAGCAGC
AGCTTCGCTTACTCTGAGGCCAGGCCCTCTCTCTCTCAGCCCCCAAGTCTCTCTCTCATCTTCTCTGGGTCTC
TCTCTCTCTCCAGGGGCTCTGTCTCTCTCTGTTCAAGCTGGGGTCCCCGATTCCAACTGTGTTTTTGGGGA
GTGTTTCCAGAGCTGCTGTGTGTCTGCTGTAAATGTTTGTCTACTGCAAGACTCTGGGCTGCCCCCTGAGCCA
GGCTCGGTACCGATCTGCTGGGCTGGGCTAGTCTCTGTCACTGTGGGCTTTGATGAGCTGATTTGCCCTTGT
CTCACCTTGACAAAGCACAGCTCTCAGAGGGCCCTCAGCCTCTCTGAGGCCCTTGTGGGACAGAACTGTGGA
CCATGCGAGTCCCGTGTGTTTCTCCATCCACACTTCAAGGACTGAGACTCTGCTTGTGTAACCTCTGGTGA
GAGCTTGAACCTCTCTTAAGAGTTCTCTCAAGGCCCAATAGCTCCAGGGCGCCCTGGCGGCCCATCATGTGT
TAACTTCTGCAAAACACACAGCGGTAGATTCTGGCTTGTGAGGTGATGGGACACAGATGACGACCATCTG
GTCACTCTCTCTGCAACACTCAGTCTGGTATGTGAGGCTGCGTGAAGCAGAACTCTGGAGCTACAGGGACA
GGGAGGCATATCTCTCTGGGAATCTGGAAGACTTCTGCGAGGCTGAGGCTTCAATCTTGACCTTGAAGAT
GGGAGGATGTTCTTTTACGTACCAATTCTTTGTCTTTTGTATTTAAAGAAAGTACATGTTTCAATTTGTAGAGA
ATTTGGAATCTGTAGAGGAATCAAGAGAAAAATAAAAAATCAGCTGTTGTAACTCGCTAGCAAAAAA
AA

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FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLQLQTLLFLLSLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIENSE
EALTVAHPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH
QEESLAQGPPLLATSVTSWWSPQNISLPSAASFTFSFHSPHTAAHNASVDMCELKRDQLL
SQFLKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEQSEIMEYSVLLPRTLQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTPVVLTFQHQQLQPKNVTLCQVFWVEDPTLSSPGHWSSAGCETVRRE
TQTSCFCNHLTYFAVLNVSSVEVDVHKKHYLSLLSYGCVVSALACLVTIAAYLCSRVP LPC
RRKPRDYTIKVHNMNLLLAFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY
PSMCWIRDSLVSYYITNLGLFSLVFLFNAMLATMVVQILRLRPHTQKWSHVLTLLGLSLVLG
LPWALIFFSFASGTFQLVVLYLFSIITSFQGFLLIFIWWSMRLQARGGPSPLKSNDSARLP
ISSGSTSSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA
GGAAANCNTCGGGACTACACCNTCAAGTGACATGAACCTGCTGCTGGCCGCTCTCCTGCTG
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCTGGATGGGCCCTCGAGGGG
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCTTGGCTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCTT
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT
GGTGTTTCTGTTCAACATGG

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FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCAGGTCAGGTTTTGCTTTGA
 TCCTTTTCAAAAATCGGAGACACAGAAAGGGCTCTAGGAAAAAGTTTGGATGGGATTATGTGGAAATACCCCT
 GCGATTCTCTGCTCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCTCGGCGGTGGTGAAGAGAC
 TCGGGAGTCGTGCTTCCAAGTGCCCGCGTGAAGTGCCTTCCACCCAGTGCAGCCTTGGTGTCTTACTGTCTTACTAA
 TTCTCTCTGCTGACATCTGCCCTGGCGCGGACAGAGGAGTGCAGGCGGACTCAGGCGGAATCCAACTCTGATGATGATTAATTC
 AGTTTTTCAGCAACCAAGGACAGAGGAGTACAAGATCCTCAGCATGAGAGAAATATTTACTGTGTCTTACTAA
 GAAGTATTTCAGCAGCCAGGTTTCTCTATCATTTATCCAGAAATACGGTCTTGGTATGAGATTTAGTAGCAGTAG
 AGGAAATGTATGATACACTTACGTTTGTATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGT
 ATGATTTTGTAGAAGTTGGAGAACCCAGTGCATGGAACTATATTAGGGCGCTGGTGTGGTCTCTGGTACTGTACAG
 GAAAAAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGTAACACAGGCT
 TCTGCATCCACTACAACATTTGTCTATGCCAATTCACAGAAGCTGTGAGTCTTCTCAGTGTCTACCCCTTCTCAGCTT
 TGCCACTGGACCTGCTTAATAATGCTATAAATGCTTGGCACTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACAG
 AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAAGCTTGGCACTTCTTGGCAAGGCTTTTGTTTTGGAA
 GAAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTTATACAGTGCACACCTCGTAACCTTCT
 CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCTTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTG
 GTGGGAACGTGTGCTTGTCTCCACAATTTGCAATGAATGTCAATGTGTGCCAAGCAAGTTACTAAAAAATACC
 ACGAGTCTCTCAGTTGAGACCAAAAGACCGGTGTGAGGGGATTGCAAAATCACTACCCGACGTGGCCCTGGAGC
 ACCATGAGGAGTGTGACTGTGTGTGAGAGGGAGCAGGAGGATAGCCGATCACCACAGCAGCTCTTGCCCA
 GAGCTGTGAGTGCAGTGGCTGATTCTATTAGAGAACGATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGTCT
 TCAAGGACCTTTTCATCTTCAAGATTTACAGTGCATTTCTGAAAGAGGAGACATCAACAGAAATTAGGAGTTGTGCA
 ACAGCTCTTTTGAAGAGGAGGCTTAAAGGACAGGAGAAAAGGTTCTCAATCGTGGAAAGAAAATTAATGTTGTAT
 TAAATAGATCACCAGCTAGTTTCAAGTTTACCATGTACGTATTTCCATAGCTGGGTTCTGTATTTCAAGTCTTTT
 GATACGGCTTAGGTTAATGTGAGTACAGGAAAAAACTGTGCAAGTGAACCTGATTTCGGTTGCCTTGTCTTAA
 TCTAAAGCTCCATGCTCTGGGCTTAAATCGTATAAAATCTGGATTTTCTTTTCTTTTGTCTCATATCACAT
 ATGTAAACCAAGACATTTCTATGTACTACAAACCTGGTTTTTAAAGGAACTATGTGCTATGAATTAACCTTGT
 GTCATGTGATAGGACAGACTGGATTTTTCATATTTCTTATTAATAATTTCTGCCATTTAGAAGAGGAGAACTACA
 TTTCAATGTTTGGAGAGATAAAACCTGAAAGAGAGTGGCCTTATCTTCACTTTTATCGATAAGTCAGTTTATTTG
 TTTCAATGTTGACATTTTATAATCTCCCTTTTGAATATAAATGTTGGCTTTTCAATCTTGTGTTAAATATATCT
 ATTTTTCACAAAGGTATTTAATATCTTTTATGACAACTTAGATCRACTATTTTGTAGCTGGTAAATTTTCT
 AAACCAATTTGTTATAGCCAGAGGAAACAAAGATGATATAAATATTTGTGCTCTGACAAAAATACATGATTTTCT
 TTTCTGATGGTCTAGAGTTAGATTAATCTGCATTTTAAAAAATGAATTTGGTATGAAATTTGGTAAAGTTGCAAA
 GAGCTTTTGAATAATTAATTAATCATATCTTCCATTTCTGTTATTCGAGATGAAATTAAGCAAGATTTATGA
 AAGTAGACATCTCAGATCCAGCAGTACTTAACCTATCTCTTTTGGGAAATCTGAGCTGAGGACCAAAACAT
 AAAGCAACCTTGAANAAGACTTGGCAGTCTTCTGATAAAGCGTGTCTGTGCTGAGGAGGAAACACATCTATTTA
 TTCTGATGTTGTGGTTTTATATCTTAAACTCTGTCCATACACTTGTATAAATACATGGATATTTTATGTACA
 AAGATATGCTCTTCAACAGTTCACTTATTGTACTCTGGCAATTTAAAGAAAAATCAGTAAAAATTTTGTCTGT
 AAAATGCTTAATATNGTGCCTAGGTTATGTGTGACTATTGTAATCAAAAATGTATTGAATCATCAATAAAGGA
 ATGTGCTATTTTGGGAGAAAAATTAAAAAAAAAAAAAAAAAAAGGTTTAGGGATAACAGGGTAAATGCGGCC

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FIGURE 207

MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITEEVRLY
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSPKVTKKYHEVLQ
LRPKTGVRGLHKSLTDVALEHHEECDVCVRGSTGG

Signal sequence:

amino acids 1-14

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FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTGCTCTCTTCAACCAGACCTCTACATTCATTTCGGAAGA
 AGACTAAAAATGGTGTTCCTCAATGTGGACACTGAAGAGACAAATCTTATCCTTTTAAACATAATCCTAAATTC
 AAATCCCTTGGGGCTAGATGGTTTCTCAAACCTCTGCCCTGTGATGTCTACTCTGGATGTTCCAAAGAACCATGTG
 ATCTGGAGCTGCACAGACAAGCAATTTGACAGAAATTTCTGGAGTATTTCCCAAGAACACACAGAACTCCACCTC
 ACCATTAACACATACAGACAATCTCCCCAGCGTCTTTTCAAGACTGGACCATCTGGTAGAGATCGATTTTCAGA
 TGCACCTGTGTACTTATTTCCACTGGGGTCAAAAAACAACATGTGCAATCAAGAGGCTGCAGATTAACCCAGAAGC
 TTTATGTGGAATCACTTATTTAAATCCCTTTTACCTGGATGGAACCAAGCTCTAGAGATAACCGAGGGCTCCCG
 CCTAGCTTACAGCTTTCTACGCTTTGAGGCCCAACATCTTTTCCATCAGAAAAGAGATCTAACAGAACTGGCC
 AACATAGAAATACTCTACTGTGGGCCAAAACCTGTTATTCGAAATCCTTGTATTTGATTTCAATAGAGAAA
 GATGGCTTCTTAACCTTTGACAAAATTTAAAGTGTCTCTCCCTGAAAGATAACATGTTCACAGCGCTCCCTACTGTT
 TTGCACTTACTTTTAAAGAACTATCTCTACAAACAACATGATTGCAAAAAATGCAAGAGATGATTTTAAATA
 CTCACCAATTAACAATTTCTGACCTAAGTGAAATTTGCCCTCGTTGTTATTAATGCCCATTTTCTTTGTGGCGCG
 TGTAAAAATAATTTCTCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGCAGAGAATTAAGTTTACGCTCTA
 CACAGTAATCTCTTTCAGCATGTGCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACCTGGATCTGTCC
 CAAAACCTCTTGGCCAAAGAAATTTGGGGATGCTAAATTTCTGCATTTTCTCCCGAGCTCATCAATTTGGATCTG
 TCTTTCAATTTTGAACCTTCAGGTCTATCTGCTCATCTGAATCTATCAAGCATTTTCTTCTACTGAAAAGCCTG
 AAAATTTCTGGGATCAGAGGATATGCTTTAAAGAGTTGAAAGCTTTAACTCTCGCCATTAATAATCTTCAA
 AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAATTTGCTAACCTCAGCATGTTTAAACAAATTTAAAGA
 CTGAAAGTCAATAGATCTTTCAGTGAATAAAATCACTTTCAGGAGATTCAGTGAAGTTGGCTCTGCTCAAAAT
 GCCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCCTGGAACAATTAATTTTTCAGATATGATAAGTATGCA
 AGGAGTTGCAGATTTCAAAAAACAAGAGGCTTCTTTCTGCTGTGTTAATGAAAGCTGCTCAAGATGGGCGAGAC
 TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTTCAGCATCTTTCTTCTCTCAATGGCCTG
 AATCTGTCAAGAAATCTCATTTAGCCAACTCTTAATGGCAGTGAATTCACACCTTTAGCAGAGCTGAGATATTTG
 GACTTCTCCAACAACCGGCTGATTTACTCCATCAACAGCATTTGAAGAGCTTCACAACTGGAAGTTCTGGAT
 ATAAGCAGTAATAGCCATTAATTTTCAATCAGAAGGAATTAATCTATATGCTAACTTTCCAAAGAACCTTAAAGTT
 CTCGAGAACTGATGATGAACGCAATGACATCTCTTCTCCACAGCAGGACCATGGAGAGTGAATCTCTTAGA
 ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTATGGAGAGAAGGTGATAACAGATCTTACAAATTTATCAAG
 AATCTGCTAAATTTAGAGGAATTTAGACATCTTAAAAATTTCCCTAAGTTTCTTGCTCTTGGAGTTTGTGATGGT
 ATGCCCTCAATTTAAGAGATCTCTCTTTGGCCAAAAATGGGCTCAAACTTTTCAAGTTGGAAGAACTCAGTGT
 CTAAGAACCTTGAAGAACTTTGGACCTCAGCCACAACCACTGACCACTGTGCCCTGAGAGATTTTCAACATGTCTC
 AGAAGCTTGAAGATGTGTTCTTTTGCATATAATCGTTTCTGTCACCTGTGATCTGTGTTTGTCTGGTGG
 GTTAACCATACGAGAGGACTACTATTTCTTACCTGGCCACAGATGTGACTGTGTGGGCCAGGACACACAAGGGC
 CAAAGGTGATCTCTCTGATCTGCTACACCTGTGAGTTAGATCTGAACCTGTATCTGTTCTCACTTTCCATA
 TCTGTATCTCTTCTTCAATGTGATGATGACAGCAAGTCACTCTATTTCTGGGATGTGTGATATATTACCAT
 TCTGTAAAGCCAAAGATAAAGGGTATCAGCGCTCTAATAACACAGACTGTGCTATGATGCTTTTATGTGAT
 GACACTAAAGCCCAAGCTGTGACCGATGGGTTTGGCTGAGCTGTGTGGCCAACTGGAAGACCCAGAGAGAAA
 CATTTTATTTATGTCTCGAGGAAGGGACTGGTTACAGGGCAGCCAGTTCTGGAAGAACTTTCCACAGAGCATA
 CAGCTTAGCAAAAAAGACAGTTTGTGATGACAGACAAGTATGCAAGACTGAAATTTTAAAGATAGCATTTTAC
 TTGTCCTCCATCAGAGGCTCATGGATGAAAGATTTGATGTGATTTATCTGATATTTCTGAGAAGCCCTTTCAAG
 TCAAGTTCTCTCAGCTCGGAAAGGCTGTGGGAGTTCTGCTGTGAGTGGCCACAACCCGAGCTCAC
 CCATACTTCTGGCAGTGTCTAAGAGAACGCCCTGGCCACAGACAATCATGTGGCCTATGATCAGGTGTTCAAGGAA
 ACGGTCTAGCCCTTCTTGCAAAACAACCTGCCCTAGTTTACAAGGAGGCGCTGGC

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FIGURE 209

MVFPMWTLKRQILILFNIIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG
IPTNTNTNLTLTINHIPDISPASFHRLDHLVEIDFRNCNCVPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSILYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYRR
NPCYVSYSIEKDAFLNLTCLKVLSLKDNNTAVPTVLPSTLTLEYLYNNMIAKIQEDDFNNL
NQLQILDLSGNCPCRCYNAPPFCAPCKNNSPLQIPVNAFDALTELKVLRLHNSLSLQHVPPRWF
KNINKLQELDLSONFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSSLKSL
KILRIRGYVFKELKSFNLSPLHNLQNLVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGO
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVQLKMMNDNDISSSTSRTMESSES
LRTLFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSL
AKNGLKSFWSKKLQCLKNLETLDLDSHNQLTTVPERLSNCSRSCLKNLILKNNQIRSLTKYFLQ
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDVWVFWVWNHTEVTIP
YLATDVTVCVPGAHKGQSVISLDLYTCBLDLTNLILFSLSISVSLFMMMTASHLYFWDVW
YIYHFCKAKIKGYQRLISPCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNCLLEE
RDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHPIFWQCLKNALATDNHVAYSQVFKETV

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 840-860

FIGURE 210

GGGTACCAATCTCTGCGCTGCTGCAAGTTACCGGAATTGAAAAATTAGAACAACAGAAAACTGGAAAACTGTTCTTC
AGTCGTCAATGCTGACCTGCAATTTTCCTGCTAATATCTGGTTCTCTGTGAGTATTGCGCGAAGAAAAATTTTCTA
GAGACTATCTCTGTGATGAGAAAAAGCAAAATGACTCAGTTATTGTCAGAGTGCAGCAATCTGCTGACTCAGGAAG
TTTCCCACCAACGCTGGGCAATATGTGACAGAACTAGACCTGTCTGATATTTTCATCAACAATACGAATGAAT
CATTTCAAGGGCTCGAAAAATCTCATAAAAATAAATCTAAACCAACAACCCCAATGTACAGCACCAGAGACGGAAATC
CCGGTATACAAATCAAATGGCTTGAATATACAGACGCGGGCAATCTCAACCTAAGAAACCTAAGGGAGTTACTGC
TCGTCAACCAACAGTTACCCCAAAATACCTCTGGTTTGGCAGAGCTTTTGACAGAACTTAGTCTTAATCAACAA
ATATATACAACTAATCAATGAAGAGGGCATTCAAGACTTATAAATCTGAAAAATCTCTATTGGCTGGAACTGCT
ATTTTAAACAAAGTTTTCGAGAAAACTTAACATAGAAGTGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTAT
CACTATCTTTCAATTTCTCTTTCAACGCTGCCACCCAACTGCCAAGCTCCCTAGCGAACTTTTCTGAGCAACA
CCAGATCAAATACTATTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACTACTAGATTAAAGCGGAACT
GTCCGAGGTGCTTCAATGCCCCATTTCATGCGTGCTTTGTATGGTGGTGCTTCAATTAATATAGATCGTTTGT
CTTTTCAAACTGACCCCACTTCGATACCTTAAACCTCTCTAGCACTTCCCTCAGGAAGATTAAATGCTGGCTGGT
TTAAAAATATGCTCATCTGAAGGTGCTGGATCTGAAATCAACTTTAGTGGGAGAAATAGTCTCTGGGGCAT
TTTTAAGCATGCTGCCCGCTTAGAAAACTTGAATCTGCTTTTAACTATATAAGGGGAGTTATCCACAGCAT
TTAATATTTCCAGAAATCTCTTAAACTTTTGTCTCTACGGGCATTGCAATTAAGAGGTTATGTTTCCAGGAAC
TCAGAGAAGATCTTTCCAGCCCTGATGCAAGCTTCCAACTTATCGACTCAACTGGGTATTAATTTTATTA
AGCAAACTGATTTCAAATCTTTCCAAATTTCTCCAATCGAAATTTATTAATCTGTACAGAAACAGAAATACAC
CGTGGTGAAGAAGTACCCCGCAGGTTATGCAAAATAGTCTCTTTTCAACGCTGATCCGGAAACGACGCTCAA
CAGATTTTGATTTGACCCCACTTGAACCTTTTATCAATTCACCCGCTCTTAATAAAGCCAAATGTGCTGCT
ATGGAAAAGCTTAGATTAAAGCTCAACAGTATTTCTTCAATGGGCCAAACCAATTTGAAATCTTCTCGACA
TCCGCTGTTTAAATCTGTCTGCAAAATGCAATGCTCAAGTGTAAAGTGAACGAAATTTTCAGCCATCTCTCATG
TCAAATATTTGGAATTTGACAAACATAGACTAGACTGTTGATTAATGTAGTCTTACTTGAATTTGCTCGCATGG
AAGTCTTAGATCTCAGACTATAATTCACACTATTTCAAGATAGCAGGCGTAACACATCATAGAATTTTATCAAAA
ATTTCAAAATCTTAAAGTTTAAACTTGAGCCACACAACTTATACCTTTACAGATAGAATTAACCTGGGAAAG
GCAAGTCCCTGGTAGAATTAGTTTTCAGTGGCAATCGCCTTGACATTTTGTGGATGATGATGACCAACAGGATA
TCTCATTTTCAAAGCTTCAAGAACTGACACGCTCGGATTTATCCCTTAATAGGCTGAGGACATCCCAAATG
AAGCATCTCTTAATTTGCGCAGCGAGTCTCACTGAATCATATAAATGATAAATGTGTTAAAGTTTTTTAACTGGA
CATTAATCTCCAGCGAGTTCTCTGCTCGAGTCTGACTTGAATCTCAATCTCTTAAACCAATCAACAAATCCGCACTTG
TATCTGACTTACACTTCTCCCTTCGGAACACTGCTGCTGACTGATCAACAGGATTTCCCACTACCTCTGCTGCTT
TTTTGAAGTCAGTAGTCTGAAGCACTCGATTTAAGTTCCAACTCTCTTAAACCAATCAACAAATCCGCACTTG
AAACTAAGACCAACCAAAATTTATGTTGGAACTACACGGAACCCCTTTGAATGCACTGTGACATTTGAG
ATTTCCGAAGATGGATGGATGAACATCTGAATGCAAAATTTCCAGACTGGTAGATGTCTATTGTGCGAGTCTG
GGGATCAAGAGGGGAGAGTATGTGAGTCTGGAGCTTAACAACTTGTGTTTTCAGATGTCACATGCACTGATAT
TTTTCTTCAAGTCTTTTATCACCACATGGTTATGTTGGCTGCCCTGGCTCACCATTCTTTACTGGAGTGT
GGTTTATATATAATGTGTTTAGCTAAGGTAAAGGCTACAGGCTCTTTTCCCAATCCCAATCTTCTATGATG
CTTACATTTCTTATGACACCAAGAGTGCCTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACACCTGGAAG
AGAGCGAGACAAAAAGCTTCTCTTTGCTAGAGGAGAGGGATTGGGACCCGGGATTTGGCCATCATGCAACCC
TCATCGAGACATCAACCAAGACAGAAAAAGTATTTGTTTAAACAAAAAATGCAAAAAAGCTGGAACTTTA
AAACAGCTTTTACTTGGCTTTGACAGGCTAATGGATGAGAACATGGATGTGATTATTTTATCTCTGGAGC
CAGCTTTTACAGCATCTCAGTATTTGAGGCTACGGGACGGGATCTGAAGAGCTCCATCTCCAGTGGCTTGACA
ACCCGAGGCGAAGAGGCTTGTTTTGGCAAACTCTGAGAAATGTGGTCTTGACTGAAATGATTTACGCGTATAAC
ATATGTATGTGCAATCCATTAAGCAATACTAATGACGTTAAGTCATGATTTCCGCGCATTAATAAGATGCAAG
GAATGACATTTCTGTATAGTTATCTATGTCTATGTAAACAAATATCCCAAACTTAGTGTTTAAACCAACCA
TTTGTCTGGCCACAGATTTTGAAGGTCAGGAGTCCAGGCCAGCAATACTGGTCTCTGCTCAGGGTGTCTCAG
AGGCTGCAATGAGGTGTTTCAAGAGACATAGGCATCATCGGGGTCACTCATGTGGTTGTTTCTGGAATTA
ATTCCTCTGGGCTATTTGGCCAAAGGCTATCTCATGTAAGCCATGCGAGGCTCTCCCAACAGGCACTGCTTC
ATCAGACGTAGCAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAACTTTTGTGAATCGAATCAAAAAGTGAAT
ATCTCATCACTTTGGGCCATTTCTATTGTTAGAAGTAAACCAAGTCCACAGGCTCCATGGGAGTGACCCCT
TCAGTCCAGGGAAGAACAGCTGAAGCAAGATGGTGAGCTGTGATTGCTTCAGTTGATCAACTGTTAAAGCTGAT
TGACTGTCTGTCTGGATGGCTCTCTATCTTGATGATAGATTGTGAATATCAGGAGGCAAGGATCACTGTGGAC
ATCTTCAGCGTTCACATACTCTTTTCAATATCTAAGAACTTTTGGCACTGTGATGATGATGATGATGATTA
TTAAGCTGTGTTTATATTATCATATATCTATGGCTACATGGTTATATTATGCTGTGGTGGCTCGGTTTAT
TTACAGTGTGTTTCAAAATTTTCTGTTAACTATGCAATTTGAAGTTTGAAGATGAGATTTGAAGATGAGAT
ATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTAAAGATGACGCTAAATTCGAGCTTTTGGCTATA
TTGTTAATGGCCATTGCTGTAAATCTTAAATGAATGAATAAAAATGTTTCATTTTCAAAAAA

FIGURE 211

MENMFLOQSSMLTCIFILLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVPTVG
KYVTELDLSDNFITHTNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLPQIPSGLPESLTSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLLELSLSFNLSLHVPPKLPSSLRKLFLENTQIKYISEEDFKGLINL
TLLEDLSGNCPRCFNAPFFPCVPCDGGASINIDRFQNLTLQRLYNLSSTSLRKINAAWFKNM
PHLKVLDFEFNYLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINISRNFSKLLSLRAL
HLRGYVFQELREDDFQPLMQPLNLTINLGINFIKQIDFKLFQNFNSNLEIYLSNRI SPLV
KDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACLNLANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDELEV
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL
DILWNDNDRYISIFKGLKNLTRLDLSLNRKHIPNEAFLNLPASLTELHINDNMLKFFNWT
LLQQFPRLELLDLRGNKLLFLTDLSLSDFTSSLRTLLLSHNRI SHLPSGFLSEVSSLKHL DLS
SNLLKTINKSALETKTITTKLSMLELHGPNPFECTCDIGDFRRWMEHLNVKIPRLVDVICASP
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVLAALAHHLFYWDVWFYINVCLAKVK
GYRSLSTSQTTFYDAYISYDTKASVTDWVINELRYHLEESRDKNVLLCLEERDWDPLAIIID
NLMQSINQSKKTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDV IIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNMYVDSIKQY

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 826-848

FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTC CCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGGCTCGCCAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGAGGA
GCAGCTCCTGCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA
GGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT
CTGGTGTGGCAGTGGGCGGCACAGAGCACGCCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT
CCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCTCTCA
CCACCTGCGACGGGCACCGGGCTGTCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCTGCCAGGCCTCGCTACGCGTGTGCTGCCCGGCTGGAAGAGGAC
CAGCGGGCTTCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCATGCCGGAACGGAGGGA
GCTGTGTCCAGCCTGGCCGCTGCCCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA
GATGTGGATGAATGCAGTGTAGGAGGGGCGGCTGTCCCAGCGCTGCATCAACACCGCCGG
CAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAA
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGC
CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGCAGCCTCC
TGGTGCATCCTTCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTCTCCTTCTG
GAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGACTCGTGACTGCCCCAGCGCCCCAGGCTG
GACTGAGCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCCTCTTCTCCTCCCC
TTCTCTGGGAGGCTCCCCAGACCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC
CCCTGGCTACCCCCACCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAAATGAACGTGA
AAGGGCGGCCGCACTCTAGAGT
CGACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTTTATTGCACTTATAATGGTTACAAAT

097375.101601

FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAATCQPPCRNGGSCVQPGRCR
CPAGWRGDTCCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKDS

Signal sequence:

1-19

0073375.101602

FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTTCAGCTTGGCTGGGCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCAGGGGTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCCAACGGGGGCCCGGGGAGGGGAATGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATC CAGGCAGCCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCCGAGGAGCAGCTCCTGCCCTGTCCGGGGATGACTGATTC
TCCTCCGCCAGGCCACCAGAGGAGAAGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGC
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGACCCCTGTCTCCGAGTCGTTTCG
TGCAGCGTGTGTACCAAGCCCTTCTCACCACCTGCGACGGGCACCGGGCCCTGCAGCACCTAC
CGAACCATCTATAGGACCGCCTACCGCCGAGCCCTGGGCTGGCCCCTGCCAGGCCCTCGCTA
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCGCATGCCGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGTCTAGGAGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGCGAGTTACTGGTGCCAGTGTGTGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCG
ACAGGAGTGGACAGTGCATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGTCT
GGAGGAGAAGCTGCAGCTGGTGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCCGACCCCGGAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCGATCGAC
TCCCTGAGCGAGCAGATTTCTTCTCTGGAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGA
CTCTGAAGTGCAGCCAGCGCTCCAGGCTGGACTGAGCCCTCACGCCGCCCTGCAGCCCCATG
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCTCCTCTTCTCCTCCTCCCTTCTCGGGAGGCTCCCCAGACCCCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAGC
CCATGGCACAGGCCAGGCAGCCCGAGGCTGGTGGGGCCTCAGTGGGGGCTGCTGCTGAC
CCCCAGCAATAAATGAAACGTG

0073375.101501

FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKDS

Signal sequence:

1-19

0978375.101501

FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGTGTATGTGGCTTCTGGTGTGGC
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGTGTCCGGGCTCACG
GGGACCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGAGCCCTGG
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTTGGGAGGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCCAAGGGAGGG
CCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGCATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGTTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCCTCC
TTCCAGCAGCTCGGCCGATCGACTCCCTGAGCGAGCAGATTTCCTTCTTGAGGAGCAGCT
GGGGTCTCTCCTTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC
TCAGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGAAGGCCAGGCAGGGCCTTCTCTCTTCTCTCTCCCTTCTCTCGGGAG
GCTCCCCAGACCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC
CCCACTCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCCTCAGCTGAGGGAAGGTAC
GAGCTCCCTGCTGGAGCCTGGGACCCATGGGCACAGGCCAGGCAGCCCGAGGCTGGGTGGG
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAAATAAAATGAAACGTG

097375.101501

FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

0978375.101601

FIGURE 218

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTTGTTCAGGAGGAGACAGCCTCCCGCCCGGGGAG
 GACAAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCTGGGACGGTCCGTTTCTGCGGTGAGCTGCGCGCG
 AGTTTGGGTCTCCGTGTTTTCAGGCGCGCTCCCCCTTCTCGGTCTCCCTTCTCCCGTGGGCGCGTTTATCGGAGG
 AGATTGTCTTCCAGGCTAGCAATTGGACTTTTGTATGATGTTTGACCCAGCGGAGGAATAGCAGGCAACGTGAT
 TTCNAAGCTGGGCTCAGCCTCTGTTTCTCTCTCGTGAATCGCAAAACCCATTTTGGAGCAGGAATCCCATTA
TGCTGTGATGGTGGTGAGAAAGAGGTGACACGGAAATGGGAGAACTCCAGGACAGGAACCTTTTGTCTGTG
 ATGGCCCGCTCATGATGGCCCCGGGCAAAAGGGCATTTTCTACTGACCCCTTTCTCATCTCTGGGACATGTACAC
 TCTTCTTCCGCTTTGAGTGCCGCTACCTGGCTGTTTCACTGTCTCTGCAATCCCTGTATTTGCTGCCATGCTCT
 TCCTTTTCTCCATGGCTACACTGTGTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCTCGGGCGCTACAGATG
 AAGCAGCTTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGGGTGCCCGAGGGCCAGGCAACACCGCTCGTA
 TCAAGAAATTTCCAGATAAACCAACGATTGTGAAACTGAAATACTGTTACACATGCAAGATCTTCCGCGCTCCCC
 GGGCTCCCATTCGACGATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCTGGGTGGGGAATTGTG
 TTGGAAGAGGAACTACCGCTACTTCTACCTCTTCATCCTTTCTCTCCCTCTCAAACTCTATGTCTTCGCT
 TCAACATCGTCTATGTGGCCCTCAAACTCTTTGAAATTTGGCTTCTTGGAGCAATTGAAAGAACTCCTGGAACGT
 TTCTAGAAGTCTCTCATTGCTTCTTTACACTCTGGTCCGTCTGGGACTGACTGGATTTCATACTTTCTCGTG
 CTCTCAACAGCAACCAATGAAGACATCAAAGGATCATGGAACAGGGAAGAATCGCTCCAGAATCCCTACAGCC
 ATGGCAATATTGTGAAGAACTGCTGTGAAGTGTGTGTGGCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTA
 TTTTGCCACTGGAGGAAAGTGAAGTGCAGCTCCAGTACTCAAGAGACAGTAGCAGCTCTTTGCCACAGAGCC
 CAGCCCCACAGAACACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG
 AGCCCCAGAGCCACCAAGGAGGAGCTGAAGCTGAGAAGTAGCCTATCTATGAAGAGACTTTTGTTTGTGTT
 TAATTAGGGCTATGAGAGATTTCAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAAT
 GTTTTCTTTGGTCTTTAGTCACCAGTGTGCACACTGGCATTTTCTGTCTGCAAGCTTTTATAAATTTCTGAACT
 CAAGGCAGTGGCAAGATGTCACTCACCTGTGATAACTGGAATAATGGGTCTCTTGGGCCCTGGCACTGGTTCT
 CCATGGCTCAGGCAACAGGGTCCCTTGGACCCCTCTCTTCCCTCAGATCCAGGCCCTCTGTCTGGGGTCA
 TGGTCTCATTCTGGGGCTAAAGTTTGTGAGACTGGCTCAAATCTCCCAAGCTCTGACGTCTGAGTCCAGAG
 GGCAGTCAAGAGACCTCTCGGCCAGGGGATCTCAACTGGGTCTTGGGGTCTTTCAGGACTGAAGAGAGGAGAG
 TGGGTGACAGAAATCTCTCGGCCACCAAGTGCCAGCAATTGCCCCACAAATCTTTAGGAATGGGACAGTACCT
 TCCACTTGTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTGTTTTCTTTTGACTCTGCTCCCATTAGGAG
 CAGGAATGGCAGTAATAAAGTCTGCATTTTGGTCATTTCTTTTCTCAGAGGAAGCCGAGTGCTCACTTAAAC
 ACTATCCCTCAGACTCCCTGTGTGAGGCTGACAGGCGCTGAAATGCACAAATGGGAAACCAAGGCACAGAGAG
 GCTCTCTCTCTCTCTCTCTCCCCGATGTACCTCAAAAAAATAAATGCTAACAGTCTTCTCCATTAAAGCT
 CGCTGAGTGAAGGAAAGCCAGCACTGCTGCGCTCTCGGGTAACTCAACCTAAGGCTCGGGCCACCTCTGGCT
 ATGTTAACCACTGGGGGCTTCTCCAGCCCCGCTCTTCCAGCACTTCCACCGGAGAGTCCAGAGCCACTT
 CACCTGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTCAGGGAAGAAGATTTATGT
 ATTATATGTGGCTATATTCTCTAGAGCACTGTGTTTCTCTTTCTAAGCCAGGGTCCGTCTCGGATGACTTAT
 GCGGTGGGGGATGTAAACCGGAACTTTTCATCTATTGAAGGCGATTAAACTGTGCTAATGCA

0978375.101601

FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTLFLILGTCTLFFAFECRYLAV
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDAAFIEMEIEATNGAVPQGGQRP
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCOVERFDHHCPWVGNCVGKKNYRYFYL
FILSLSLTLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLI CFFTLWSVVGLTGFHTF
LVALNQTINEDIKGSWTGKNRVQNPYSHGNIVKNCCEVL CGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPPEPPQEAAEA EK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

0976375.101601

FIGURE 220

AAAACCCTGTATTTTTTACAATGCAAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTGGCTTTGGACTCTCNCTTTCT
CCCACAGAGCNCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTGTGGAAAGAGGAACTA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAAATCTATGTCTTCGCCTTCA
ACATCGT

09737E.101601

FIGURE 221

GTGTGTCTTCAGCAAAACAGTGGATTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAAAAACCGAACCTGACAAAAAGAGAAAAAGAGA
AAAAAATCATGAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCTCAGGTGCATATT
GACAACCGGGTCACCCGGGTGGCCTGAGCTAAACCGCAGCACCATCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTC
TTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACCTTGAAATTCAGGGCATACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACATCCACCATACA
TTTCAGAAGCCAAGGTTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGCCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTACGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCGGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA
AATTGCCTTGCAGATATTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCCAAGCGTGGCGCTGCGG
GACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAACGTGAAATAAAAAGAGCAAAA
AAAAA

0976375.101601

FIGURE 222

MKTIQPKMHNSISWAIFTGLAALCLFQGVFVRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNIRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVIWRHISPKAVGFVSEDEYL
EIQGITREQSGDYECASNDVAAPVVRVRKVTVNYPPIYISEAKGTGVFVGQKGTLCCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHNTNASIML
FGPGAVSEVSNGTSSRRAGCVWLLPLLVLHLLKF

Signal peptide:

amino acids 1-28

0978375.101001

FIGURE 223

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATT
TCTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

05073375.104604

FIGURE 224

ATGGCTGGTGAACGGCGGGGCGGGGACCGGGGCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
 ATCACCGCTGGCCGACTCCACCATGAACGTGCGCTGCAGGAGCTGGGAGCTGGGAGCAACGTTGGGATTCCAG
 AAGGGGACAGACAGCTGTTAGGCTCACGACACGAGCTGGAGCTGCTTACGAGGTCCTCTCTACTGCTGGCT
 GCAGTGTCTTGGGCTGCTTGTGGCCCTAGGGGTCCAGTACACAGAGACCCATCCACAGCACTGCTTAC
 GAGGCTCTGATTGGAGTGGCTGGAAAAATCTGGAGTCCCTGGACCGAGGGGTGAGCCCTGTGAGGACTTTTAC
 CAGTTCTCTGTTGGGGGTGGATTTCGGAGGAACCCCTGCCCGATGGGCGTTCTCGCTGGAAACCTTCAACAGC
 CTCTGGGACCAAAACGAGCCATACTGAAGCACCTGCTTGAAAAACCACTTCAACTCCAGCAGTGAAGCTGAG
 CAGAAGACACAGCGCTTCTACTTATCTTGCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGA
 GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACAGGACAACCTTATGGAGGTGTTGAAG
 GCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTCACCGTCTACATCAGTGCCGACTCTAAGAGTTCRAACAGC
 AATGTTATCCAGGTGAGCAGCTGTGGGCTCTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG
 AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACGGGGATGCTGCTGGGTGGGCGGCCCACTCCAAGAGG
 GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACTCACAGTGCCCCAGGACAGCGGCGCGAC
 GAGGAGAAGATCTACCAAGATGAGCATTTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTT
 CTGTCTTTCTGTCTGCACCATTTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
 CAGGTGTGAGAGCTCATCAACCGCAGGAAACCAAGCATCTGAAACAATTACCTGATCTGGAACTGGTGCAGAAAG
 ACAACCTCAAGCCTGGAGCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCTCTATGGCACTAAGAAG
 TCCTGTGTGCCAGGTGGCAGACCTGCATCTCCAACAGGATGAGCGCCCTGGCTTTGCTTTGGGGTCACTCTTC
 GTGAAGGCCAGCTTTGACCGGCAAGCAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAG
 GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCGAGGCGAGCAAGGAGAAAGCAGATGCCATCTAT
 GATATGATTTGTTTCCAGACTTTATCTCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
 GAAGATTCTTCTTCCAAAACTGTTGAATTTGTACAACCTCTCTGCGAAGGTTATGGCTGACAGCTCCGCAAG
 CCTCCAGCGCGAGACCATGGAGCATGAACCCCGAGACAGTGAATGCCACTACTCTCAACTAAGAATGAGATC
 GTCTCCCGCTGGCATCTCTGAGGCCCCCTTCTATGCCCGCAACCAACCCAGGCCCTGAACTCTCGTGGCATC
 GGTGTGGTCACTGGGCCATGAGTTGACGCTATGCTTTGATGACCAAGGCGCGAGATGAGCAAGAAAGGAACCTG
 CGCCCTGGTGAGAAATGAGTCCCTGGCAGCCTTCGGAACCAAGGGCTGCTATGGAGGAACAGTACAATCAA
 TACCAGTCAATGGGAGAGGCTCAACGCGCCGCGAGAGCTGGGGAGAGCACTTACTGACAACGGGGGGCTGAAG
 GCTGCTCAATGCTTACAAGACATGGCTGAGAAAGCATGGGAGAGAGCACTGCAAGCCGTGGGGCTCACC
 AACCAACAGCTCTTCTCGTGGGATTGCGCAGGTGTGGTGTCTCGTCCGCAACACAGAGAGCTCTACAGAGGG
 CTGGTGACCGACCCCAAGCCCTGCCCGCTTCGCGTGTGGGCACTCTCTCAACTCCCGTGACTCTCTGGG
 CACTTCGGCTGCCCTGTGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACTGGATCAGGGGA
 GAAATGGCCAGCTGTCAACCACTGGGCGAGCTCTCTGACAAAGCTGTTTGTCTCTGGGTGGGAGGAAGCAA
 ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCACAGGTGACATGAGTACAGAGCCTCTCTCAATCACCACATGT
 TGCTCTGCTTTGGGGGTGCCCTGCCCTCAGCAGAGGCCCCACCAATTCACTGTGACATCTTTCGTGTACCCCT
 GCTTGAAGAGGTCTGGGTGGGAGGCCAGTTCCCATAGGAAGAGTCTGCC

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FIGURE 225

MNVALQELGAGSNVGFQKGTQRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH
STCLTEACTRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLDGRSRWNTFNSLWDQNQA
ILKHLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLEIKIGWNI TGPWDQDN
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLFSPRDYYLNRTANEKVL TAY
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEKLETTYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTAFEELGQLVWMDKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNLMLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLP TKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS
VRTPESSEHGLVTDPHSPARFVLGTLSNSRDFLRHFGCPVGSPMNPQGQLCEVW

Type II Transmembrane domain:

amino acids 32-57

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FIGURE 227

GGCCGAGCGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCCTGGCCCCGAC
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAAGG
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCACAGCACCTGCCTTACAGAGGCGCTGCATTTCAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCCGTGTGAGGACTTTTACCAGTTCTCCTGTGGGGCTGGATTCCGA
GGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTCTTCAC
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAAGTCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAAATGCCCTT
CCTTTCTTTCTTTCTTTCTTCTCCTCCCTCCCTCCCTTTCTTCCCTTTTCTTCTTCTTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTTCG
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTTCAGTGTGATGGGTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTACAGGAGAGACTTATGGAGCC
AGCAAAGTCTTCTGAAAGAGATTGCATTGAGCCAGGTCTGTAG

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FIGURE 228

ATGCCTACTACCTTCCAAC TAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC
TTCTATGCCCGCAACCACCCCAAGGCCCTGAAC TTCCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACTGCGGC
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACGCGCTGCATGGAGGAACAG
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAA CTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAAC TCCCGTGACTTCTGCGGC
ACTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA
GGTGACATGAGTACAGACCCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCT
GCCTCCAGCAGAGCCCCACCATTCACTGTGACATCTTTCGTGTCAACCTGCCTGGAAGAG
GTCTGGGTGGGAGGCCAGT TCCCATAGGAAGGAGTCTGCCCTCTTCTGTCCCAGGCTCACT
CAGCCTGGCGGCCATGGGGCTGCCGTGCCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCACCTTAGGGGTGGACTCAGCTCTGTC
TGGCTCACCTCACGGGCTACCCCCACCTCACCTGTGCTCCTTGTGCCACTGCTCCCATG
CTGTGCTGACCTTCACTGACAGCTCCTAGTGAAGCCCAAGGGCTCTGAAAGCCTCCTGC
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCAATATGTGTAGCGGTACTGGTTCTGT
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA
GAGCAGGGAAGGAAGAAGACAGAGTTTATTTTACAGAAAAGAGGTGGGAGGGTGTGGTCT
TGGCCCTTATAGGACC

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FIGURE 229

CCCACGCGTCCGAGCCGCCGAGAAATTAGACACACTCCGGACGCGGCCAAAAGCAACCGAGA
 GGAGGGGAGGCAAAAACACCGAAAAACAAAAGAGAGAAACAACACCCCAACTGGGGTGG
 GGGGAAGAAAGAAAGAAAAGAAACCCACCCACCCAAAAAAGAAAAAAGAAAAA
 AAAAAAAGAAATCCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTCGCCAGCACCAGGGGG
 TGGGGAGTGCAGAGCTGAAAGCTGCTGGAGAGTGAAGCAGCCCTAGCAGGGATGGACATGATG
 CTGTTGGTGGAGGGTCTGTTTGGCTCGAACCCAGTGGCTGGCGGGTGTCTCCTCAGCCTGTG
 CTGCTGTCTACCTCTGCTCCTCCGGCTGGACAGAGTGTGGACTTCCCTGGGCGGCGGTGG
 ACAACATGATGGTGCAGAAAGGGGACACGGCGGTGCTTAGGTGTATTTGGAAGATGGAGCT
 TCAAAGGGTGCTGGCTGAACCGGTCAAGTATTATTTTTCGGGAGGTGATAGTGGTCACT
 GGATCCTCGAGTTTCAATTTCAACATTGAATAAAGGGACTACAGCCTCCAGATACAGAATG
 TAGATGTGACAGATGATGGCCCATACACGTGTTCTGTTACAGACTCAACATACACCCAGAACA
 ATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC
 CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGTTGGCCACTGGGAAACAGAGCCTTCCA
 TTTCTTGGCGACACATCTCCCCATCAGCAAAACCTTTGAAATGGGACAATATTTGGACATT
 TATGGAATTTACAGGGACACAGGCTGGGGAAATATGAATGCAGTGCAGGAAATGCTGTGTCACT
 CCGAGATGTGAGGAAAGTAAAGTGTGTGTCACACTTTGCTCCTACTTTTTCAGGAATTAAT
 CTGGCACCGTGACCCCGGACGCGAGTGGCTGATAAGATGTGAAGTGCAGGTGTGCCGCT
 CCAGCCTTTGAATGGTACAAGAGGAGAGAAGAGCTCTCAATGGCCAACAAGGAATTTATAT
 TCAAAATTTTACACAGAGTCCATTTCTCACTGTACCAACGTGACAGGAGCACTTTGGCA
 ATTATACCTGTGTGGCTGCGCAACAGCTAGGCACAAACCAATGCAGCCTGCCTTTAACCT
 CCAAGTACAGCCAGTATGGAATTACCGGAGCGCTGATGTTCTTTTCTCTGCTGGTACCT
 TGTGTTGACAGTGTCTCTTTTCCACGACATATTTCTACCTGAAGAATGCCATTCTACAATAAA
 TTCAAAGACCCATAAAGGCTTTTAAGGATTCTCTGAAAGTGTGATGGCTGGATCCAATCT
 GGTACAGTTTGTAAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGATGATCGCC
 TTCTGTAGAATTGCTCATTATGTAAATACTTTAATTTACTCTTTTGTATTAGCTACATTA
 CCTTGTGAAGCAGTACACATTGTCTTTTAAAGACGTGAAAGCTCTGAATTAATCTTTTAG
 AGGATATTAATTGTGATTTTCATGTTTGTAACTACAACCTTTCAAAGCATTCACTCATGGT
 CTGCTAGGTGTCAGGCTGTAGTTTACAAAAACGAATATTGCAGTGAATATGTGATCTTTAA
 GGCTGCAATACAAGCATTCACTTCCCTGTTTCAATAAGAGTCAATCCATTTACAAGATG
 CATTTTTTTCTTTTTTGATAAAAAAGCAAATAATATTGCTTCCCTCAGATTATTTCTTCAAATA
 TAACACATCTAGATTTTTCTGCTTGCATGATATTCAAGTTTTCAGGAATGAGCCTTGTAAAT
 ATAACGTGCTGTGCAGCTCTGCTTCTCTTCCCTGTAAGTTTCAGCATGGGTGTCCTTATAC
 AATAATATTTTTCTCTTTGTCTCCAATAATAAATGTTTTGCTAAATCTTACAATTTGA
 AAGTAAAAATAAACAGAGTGTCAAGTTAAACCATACACTATCTCTAAGTAACGAAGGAGC
 TATTGGACTGTAATAATCTCTCTGCACTGACAATGGGGTTTGGAATTTTGGCCCACT
 AACTCAGTTCTTGTGATGAGAGACAATTTAATAACAGTATAGTAATATACCATATGAGATTC
 TTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAATCATTCCTTTAAATGACAGCACA
 GTCCACTCAAAGGATTGCTTAGCAATACAGCATCTTTTCTTTCACTAGTCCAAGCCAAAA
 TTTTAAGATGATTTGTGAGAAAGGACAAAGTCTTATCACCTAATATTACAAGAGTTGGTA
 AGCGCTCATCATTAATTTATTTTGTGGCAGGTATTATGACAGTGCAGCTGGAGGGTATGGA
 TATGATATGGACGTTCCAGAGACTATAATGGCAGAAACAGGGTGGTTATGACCGCTACTC
 AGGAGGAATTCAGAGACAATTATGACAACTGAAATGAGACATGCACATAATATAGATACA
 CAAGGAATAATTTCTGATCCAGGATCGTCTTCCAAATGGCTGATTTTGAAGTTTGG
 AGCTGCACTGAAGCATCTTATTTTATAGTATATCAACCTTTTGTTTTAAATTTGACCTGCCA
 AGGTAGCTGAAGACCTTTTAGACAGTTCCATCTTTTTTTTTTAAATTTTTTCTGCTCATTTAA
 AGACAAATTAGGGACGTTTGTCAAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 230

MMLLVQGACCSNQWLA AVL LSLCCLLPSCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYLED
GASKGAWLNRSSII FAGGDKWSVDPRVSISTLNKRDYSLQIQNV DVTDDGPYTCSVQTQHTP
RTMQVHLTVQVPPKIYDISNDMTVNEGTNVTLTCLATGKPEPSISWRHISPSAKPFENGQYL
DIYGITRDQAGEYEC SAENAVSFPDVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGV
PPPAFEWYKGEKKLFNGQQGGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGT TNASLPL
NPPSTAQYGITGSADVLFSCWYLVLTLS SFTSIFYLKNAILQ

Important features of the protein:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 326-345

N-glycosylation sites.

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

Casein kinase II phosphorylation site.

amino acids 147-151, 208-212, 224-228

Tyrosine kinase phosphorylation site.

amino acids 178-186

N-myristoylation sites.

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,
302-308, 319-325

Myelin P0 protein:

amino acids 92-121

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FIGURE 231

AGTGGTTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTCTCTGCTGG
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATCTCAAGGAGGA
CGAGCTCTTGAGTGAGACCAACAAGCTGCTTTTACCACAAATGCAATGGAGCCTTTTCGAAA
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACTTCTCCCTAGCTGTGGTGGTCATC
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC
GCGGCTCCGGGTCTCTGGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT
CCTTCTCCTTGCTGCAGTCAGCACACCCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTG
CAAGTCCTGCAGGCCCAACTCACCTGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGT
AGACAACTTCACTCAGAACCCAGGGATGTTCAGAATCAAAGGTGAACAAGGCGCCCCAGGTCT
TTCAAGGTCACAAGGGGGCCATGGGCATGCTGGTGCCCTGGCCCGCCGGGACCACTGCT
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTCGGGACCCCAAGG
CCCACCGGGAGTCAAGGGAGAGGCGGGCTCCAAGGACCCAGGGTGTCTCAGGGGAAGCAAG
GAGCCACTGGCACCCAGGACCCCAAGGAGAGAAGGGCAGCAAGGCGATGGGGGTCTCATT
GGCCCAAAAGGGGAACTGGAACTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTGAGGGCTCTGGAGCCAGGGGAGTA
AAGGTGACTTCGGGAGGCCAGGCCACCAGGTTTGGCTGGTTTTCTGGAGCTAAAGGAGAT
CAAGGACAACCTGGACTGCAGGGTGTTCGGGGCTCTGGTGCAGTGGGACACCAGGTGC
CAAGGGTGAGCCTGGCAGTGTGCTGCTCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGA
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAGGGGACACAGGACTTCAAGGACAGCAAGGA
AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCAGG
GCTGGCAGGTCCCAAGGGAGCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCC
GTCAGGATTGTGCGCAGTAGTAAACCGAGGCCGGGTGAAGTTTACTACAGTGGTACCTGGGG
GACAATTTGCGATGACGAGTGGCAAAATCTGATGCCATTGTCTCTGCCGCATGCTGGGTT
ACTCCAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCATGGGCAGATCTGGCTGGATAAT
GTTCAAGTGTGCGGGCACGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCATCA
TGACTGCAGCCACGAGGAGGACGACAGGCGTGGAGTGAGCTGAGCGCTGAGACCCGGAAACCTTTCA
CTTCTGTCTCCCGAGGTGTCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAAATAAGCTCAACATCATTGA

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FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAPHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLLITAGAGL
LVVQVLNLQARLVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR
VSHEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD
GATGPGSPQGPVVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGE
KGDGLGLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFPGAKGDDQGPGLQGVP
PPGAVGHPGAKGEPGSAGSPGRAGLPGSPGSGATGLKGSKGDGTGLQGQQGRKGESGVPGPA
GVKGEQGSPLAGPKGAPGQAGQKGDQGVKGSSEGEQGVKGEKGERGENSVSVRIVGSSNRGR
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLNDNVQCRGTESTLW
SCTKNSWGHHDCSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

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FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGCCCAAACTCACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAAGGAAAGAAGAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTAC
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACTGTCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCCCAAAAGACGTTTTCTTTGGACCAAAGATCTCTTTCG
TGATTCCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTTCCTGATTTT
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA
AGTTAATTCAATCTAAAAAAAAAAAAA

09070675.101601

FIGURE 234

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1

MKLMVLVFTIGLTLLLGVDQAMPANRLSCYRKILKDHNCNLPQGVADLTQIDVNVQDHFWDG
KGCEMICYCNFSELLCCPKDVFVFGPKISFVIPCNNQ

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-76

Tyrosine kinase phosphorylation site.

amino acids 63-71

FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGCTCTGGAGCGAATTCACGCTGCAGGG
CTGATAAGCGAGGCATTAGTGTAGATTGAGAGAGACTTTACCCCGCGTGGTGGTGGAGGGC
GCGCAGTAGAGCAGCAGCA CAGGCGCGGGTCCC GGGAGGCCGGCTCTGCTCGCGCCGAGATG
TGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCCGCTGGCTGTG
CGCTGGGGCGCTGGTGTCTGGCGGGTGGCTCTTTCTCCTCGGCTTCTCTTTCGGGTGGTTA
TAAAACTCTCCAATGAAGCTACTAACAATTACTCCAAAGCATAAATATGAAAGCATTTTTGGAT
GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCAATTAGC
AGGAACAGAACAAAACTTTCAGCTTGCAAAGCAAATTC AATCCCAGTGGAAAGAAATTTGGCC
TGGATTCTGTGTAGCTAGCTCATTATGATGTCCTGTTGTCCTACCCAAATAAGACTCATCCC
AACTACATCTCAATAATTAATGAAGATGGAATGAGATTTTCAACACATCATTATTTGAACC
ACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACACACCTTTTCAGTGCTTTCTCTCCTC
AAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACCTGAAGACTTCTTTAAA
TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTTGAATTTGCCAGATATGGGAAAGT
TTTCAGAGGAAATAAGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCAATTCTCTACT
CCGACCCTGCTGACTACTTTGCTCTCTGGGGTGAAGTCCATATCCAGACGGTTGGAATCTTCCCT
GGAGGTGGTGTCCAGCGTGGAAATATCTTAAATCTGAATGTGCAGGAGACCTCTCACACC
AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGAATTCAGAGGCTGTTGGTCTTCCAA
GTATTCCTGTTTCATCCAATTGGATACATGATGCACAGAAGCTCTTAGAAAAAATGGGTGGC
TCAGCACCCAGGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG
CTTTACTGGAACCTTTTCTACACAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA
CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAAACAGACAGATGTCATT
CTGGGAGGTCAACGGGACTCATGGGTGTTTGGTGGTATTGACCTCAGAGTGGAGCAGCTGT
TGTTTCATGAAATTTGTGAGGAGCTTTGGAACACTGAAAAGGAAGGGTGGAGACCTAGAAGAA
CAATTTTGGTTTGCAAGCTGGGATGCAGAAGAAATTTGGTCTTCTTGGTTCTACTGAGTGGGCA
GAGGAGAATTCAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT
AGAAGGAAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC
TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAGTTGG
ACTAAAAAAGTCTCTTCCCAGAGTTTCAAGTGGCATGCCAGGATAAGCAAATTTGGGATCTGG
AAATGATTTTGGAGGTGTTCTTCCAACGACTTGAATTTGCTTCAGGACAGCACGGTATACTA
AAAATTTGGGAAACAAACAAATTCAGCGGCTATCCACTATCATCAGTGTCTATGAAACATAT
GAGTTGGTGGAAAAGTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCCAGGTTTCG
AGGAGGGATGGTGTGTTGAGCTAGCCAATTCATAGTGCTCCCTTTTGATTGTCGAGATTATG
CTGTAGTTTTTAAAGATATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA
ATGAAGACATACAGGTATCATTGATTCACTTTTTTCTGCAGTAAAGAAATTTACAGAAAT
TGCTTCCAAGTTTCAGTGGAGACTCCAGGACTTTGACAAAAGCAACCCAAATGATTAAGAA
TGATGAATGATCAACTCATGTTTCTGGAAGAGCATTTATTGATCCATTAGGGTTACAGAC
AGGCCTTTTTATAGGCATGTCTATGCTCCAAAGCAGCCACAACAGTATGCAGGGAGTCA
ATTCCAGGAATTTATGATGCTCTGTTTGATATTGAAAGCAAAGTGGACCCCTTCCAAGGCCT
GGGAGAAAGTGAAGAGACAGATTTATGTTGCAGCCTTCAGTGCAGGCAGCTGCAGAGACT
TTGAGTGAAGTAGCTTAAGAGGATTTTTAGAGAATCCGATTTGAATTTGTTGGTATGTTCA
CTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAATTTGGTATATTTGAAATAAAGT
TGAATATTATATATAA

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLHETDSAVATARRRWLCAGALVLAGGFLLGLGFLGWFIKSSNEATNITPKHNMKAFI
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH
PNYISIINEDGNEIFNTSLFEPPPPGYENVS DIVPPFSAFSPQGMPEGDLVYVNYARTEDFF
KLERDMKINCSGKIVIARYGKVFRGNKVNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNL
PGGGVQQRGNILNLNGAGDPLTPGYPANAYARRGIAEAVGLPSIPVHPIGYYDAQKLEKMG
GSAPPDSSWRGSLKVPYNVGPFTGNFSTQKVKMHISTNEVTRIYNVIGTLRGAVEPDYV
ILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGLTKKEGWRPRRTILFASWDAEEFGLLGSTEW
AEENSRLLQERGVAYINADSSI EGNVTLRV DCTPLMYSLVHNLTKEKLS PDEGFEGKSLYES
WTKKSPSPESFGMPRI SKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYET
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ
EMKTVSVSFDLSFAVKNFTEIASKF SERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP
DRPFYRHHVIYAPSSH NKYAGESFPPIYDALFDIESKVDPSKAWGEVKRQIYVAFTVQAAAE
TLSEVA

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,
459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,
360-366, 427-433, 529-535, 707-713

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